

FT /note= "Encoded by GRCA"
 XX WC200060087-A2.
 PN XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PA Klein TM, Weng Z, Cahoon RE;
 XX PI
 XX DR
 PD 12-OCT-2000.
 XX WPI; 2000-679375/66.
 XX N-PSDB; AAA95286.
 PF 06-APR-2000; 2000WO-US009106.
 XX CYclin dependent kinase inhibitor sequences, useful for identifying
 PR 07-APR-1999; 99US-0128192P.
 XX PT herbicides and plant growth inhibitors.
 XX PS Claim 10; Fig 1; 58pp; English.
 XX
 CC The present sequence is the rice cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a rice seed cDNA
 CC library for sequences similar to those encoding the CDKI from Chenopodium
 CC rubrum. Cnenorhabditis elegans and Arabidopsis thaliana. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of
 CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms
 XX SQ Sequence 37 AA;
 Query Match Score 36; DB 3; Length 37;
 Best Local Similarity 75.0%; Pred. No. 2.1;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC Qy 1 FXXXKNF D 8
 Db 8 FAAKKNFD 15
 XX RESULT 6
 ID ABB98860 standard; protein; 42 AA.
 XX ABB98860
 XX AC ABB98860;
 XX DT 21-FEB-2003 (first entry)
 XX DE Maize CKI_B C-terminal protein fragment.
 XX KW Maize; cyclin-dependent kinase inhibitor; CKI; plant; corn; crop yield;
 KW root size; plant growth; tassel size; ear size; male sterility;
 KW endoreduplication.
 XX CS Zea mays.
 XX PN WO200281623-A2.
 XX XX *17-OCT-2002.
 AC AAB2252;
 AC AAB2252;
 XX DT 17-JAN-2001 (first entry)
 DE Rice cyclin-dependent kinase inhibitor #3.
 KW Rice; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division;
 KW cell growth; herbicide.
 OS Oryza sativa.
 XX Key Location/Qualifiers
 FT Misc-difference 34 /note= "Encoded by AAGC"
 FT XX WO200060087-A2.
 XX PR 12-OCT-2000.
 XX PD 06-APR-2000; 2000WO-US009106.
 XX PR 07-APR-1999; 99US-0128192P.
 XX PS Example 11; Page 46; 69pp; English.
 XX CC The present invention relates to maize cyclin-dependent kinase inhibitor

(CKI), CKI_B, CKI_C and CKI_D. The coding sequences (I) for these proteins are useful for modulating the activity of CDK in a plant such as a corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, oil-seed Brassica and millet. Modulating the activity of CDK, preferably modulating downward is useful for providing differential growth in a plant, especially a positive growth advantage and modulating CDK activity upward is useful for increasing crop yield, root size, plant growth, tassel size and/or ear size. Modulating CDK activity is also useful for conferring male sterility and for improving transformation frequencies by increasing the number of cells in cell division. CDK activity can also be modulated for modulating endoreduplication in the endosperm of corn, sorghum, wheat, rice, barley, and millet, where the promoter used is an endosperm-preferred promoter. The cell numbers are modulated in one or more tissues of a plant, comprising root, seed, tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves, stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm, pericarp, meristematic or leaf cells. (I) is also useful for identifying maize CKI interacting proteins, by addingucting the nucleic acid sequence to a second nucleic acid sequence encoding a DNA-binding domain. The present sequence is a C-terminal protein fragment of CKI_D. This sequence contains a CDK binding region and/or cyclin binding domains.

Sequence 42 AA:
 SQ Query Match 94.7%; Score 36; DB 6; Length 42;
 Best Local Similarity 75.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FXXXKNFD 8
 Db 14 FASKNFD 21

RESULT 7
 ABB98862
 ID ABB98862 standard; protein; 46 AA.
 XX AC ABB98862;
 XX DT 21-FEB-2003 (first entry)
 XX DB Maize CKI_D C-terminal protein fragment.

XX KW Maize; cyclin-dependent kinase inhibitor; CKI; plant; corn; crop yield; root size; plant growth; tassel size; ear size; male sterility; endoreduplication.
 XX OS Zea mays.
 XX PN WO200281623-A2.
 XX PD 17-OCT-2002.
 XX PP 06-NOV-2001; 2001WO-US044038.
 XX PR 07-NOV-2000; 2000US-0246349P.

XX PA (PION-) PIONEER HI-BRED INT INC.
 (ARIZ-) ARIZONA BOARD OF REBENTS.
 XX PI Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;
 DR WPI: 2003-058511/05.

XX Novel cyclin-dependent kinase polynucleotides and their encoded proteins, involved in cell cycle regulation, and useful for altering cell cycle protein content, cell cycle progression, cell number and composition of plants.
 XX Example 11; Page 46; 69pp; English.

XX The present invention relates to maize cyclin-dependent kinase inhibitor (CKI), CKI_B, CKI_C and CKI_D. The coding sequences (I) for these

proteins are useful for modulating the activity of CDK in a plant such as a corn, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, oil-seed Brassica and millet. Modulating the activity of CDK, preferably modulating downward is useful for providing differential growth in a plant, especially a positive growth advantage and modulating CDK activity upward is useful for increasing crop yield, root size, plant growth, tassel size and/or ear size. Modulating CDK activity is also useful for conferring male sterility and for improving transformation frequencies by increasing the number of cells in cell division. CDK activity can also be modulated for modulating endoreduplication in the endosperm of corn, sorghum, wheat, barley, and millet, where the promoter used is an endosperm-preferred promoter. The cell numbers are modulated in one or more tissues of a plant, comprising root, seed, tassel, ear, silk, stalk, embryo, flower, grain, germ, head, leaves, stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm, pericarp, meristematic or leaf cells. (I) is also useful for identifying maize CKI interacting proteins, by addingucting the nucleic acid sequence to a second nucleic acid sequence encoding a DNA-binding domain. The present sequence is a C-terminal protein fragment of CKI_D. This sequence contains a CDK binding region and/or cyclin binding domains.

Sequence 46 AA:
 SQ Query Match 94.7%; Score 36; DB 6; Length 46;
 Best Local Similarity 75.0%; Pred. No. 2.6;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 8
 AAB26245
 ID AAB26245 standard; protein; 53 AA.
 XX AC AAB26245;
 XX DT 17-JUN-2001 (first entry)
 XX DE Corn cyclin-dependent kinase inhibitor #1.
 XX KW Corn; cyclin-dependent kinase inhibitor; CDKI; cell cycle; cell division; cell growth; herbicide.
 XX OS Zea mays.
 XX PN WO200060087-A2.
 XX PD 12-OCT-2000.
 XX XY 06-APR-2000; 2000WO-US009106.
 XX PR 07-APR-1999; 99US-0128192P.
 XX PA (DUPRO) DU PONT DE NEMOURS & CO E I.
 XX PI Klein TM, Wang Z, Cahoon RE;
 XX DR WPI: 2000-679175/66.
 XX N-PSMB; AAA95276.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying PT herbicides and plant growth inhibitors.
 XX PS Claim 10; Page 40; 58pp; English.

XX The present sequence is the corn cyclin-dependent kinase inhibitor (CDK). Its coding sequence was isolated by searching a corn silk cDNA library. For sequences similar to those encoding the CDK from *Cheropodium rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*, CDK is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of

CC transgenic plants which produce increased or decreased amounts of the
 CC CDK1 protein, in the identification of herbicides, in genetic and
 XX physical mapping and in the isolation of the CDK1 gene in other organisms

SQ Sequence 53 AA;

Query Match	94.7%	Score	36;	DB	3;	Length	53;
Best Local Similarity	75.0%	Pred.	No.	3;			
Matches	6;	Conservative	0;	Mismatches	2;	Indels	0;
						Gaps	0;

Qy 1 FXXXYNFD 8
 Db 30 FASKYNF D 37

RESULT 9

AAP01940

ID AAP01940 standard; protein; 53 AA.

XX

AC AAP01940;

XX

DT 01-NOV-2001 (first entry)

XX Corn Cyclin dependent kinase inhibitor (CDK1) clone csi1n.pk0050.e6.

DE

XX Cyclin dependent kinase inhibitor; CDK1; herbicide; cell cycle; corn;

KW

XX plant growth inhibitor.

XX

OS Zea mays.

XX

PN WO200060087-A2.

XX

PD 12-OCT-2000.

XX

PP 06-APR-2000; 2000WO-US000106.

XX

PR 07-APR-1999; 9US-0128192P.

XX

PA (DU PONT DE NEMOURS & CO E I.

XX

PI Klein TM, Weng Z, Cahoon RE;

XX

WPI: 2000-679375/66.

DR N-PSDB; AAN02390.

XX

FR Cyclin dependent kinase inhibitor sequences, useful for identifying

XX

PT herbicides and Plant growth inhibitors.

XX

Claim 10: Page 40: 5BPP; English.

XX

The invention describes a novel isolated polynucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDK1) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDK1 polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDK1 or effects the level of CDK1 expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDK1. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the corn CDK1 clone csi1n.pk0050.e6 as described in the method of the invention

XX

SQ Sequence 53 AA;

Query Match	94.7%	Score	36;	DB	3;	Length	53;
Best Local Similarity	75.0%	Pred.	No.	3;			
Matches	6;	Conservative	0;	Mismatches	2;	Indels	0;
						Gaps	0;

Qy 1 FXXXYNFD 8

Db 30 FASKYNF D 37

RESULT 10

ABG65674

ID ABG65674 standard; protein; 116 AA.

XX

AC ABG65674;

XX

DT 07-AUG-2003 (revised)

XX

DE Corn ICK 1 protein.

XX

Plant; inhibitor of cyclin dependent kinase; ICK.

XX

OS Zea mays.

XX

PN WO200228893-A2.

XX

PD 11-APR-2002.

XX

DT 29-JUN-2001; 20001WO-IB001492.

XX

DE Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used

XX

PT to screen substrates, drugs or compounds which modulate ICK activity and

XX

PT treat disorders characterized by an insufficient or excessive production

XX

PT of ICK inhibitors.

XX

PA (CRO-P-) CRODESIGN NV.

XX

PI Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

XX

PI Hatzfeld Y;

XX

WPI: 2002-471311/50.

XX

DR N-PSDB; ABK93954.

XX

PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used

XX

PT to screen substrates, drugs or compounds which modulate ICK activity and

XX

PT treat disorders characterized by an insufficient or excessive production

XX

PT of ICK inhibitors.

XX

PA (ICK) protein of the invention. (Updated on 07-

XX

Sequence 116 AA;)

CC This invention relates to the DNA and protein sequences of novel isolated

CC ICCK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of

CC the invention may be used for treating disorders characterised by

CC insufficient or excessive production of an ICCK inhibitor. The protein of

CC the invention may also be used to screen for naturally-occurring ICCK

CC substrates, drugs or compounds which modulate ICCK activity, as well as to

CC treat disorders characterised by insufficient or excessive production of

CC ICCK protein, forms which have decreased or aberrant activity compared to

CC ICCK wild type protein. The present sequence represents an inhibitor of

CC cyclin dependent kinase (ICK) protein of the invention. (Updated on 07-

XX

Sequence 116 AA;)

CC

CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention

XX Sequence 226 AA;

Query Match 94.7%; Score 36; DB 5; Length 226;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXXYNFD 8
 Db 196 FAXKYNFD 203

XX RESULT 14

ID ABB98757 standard; protein; 256 AA.
 XX ABB98757;

AC ABB98757;

DT 21-FEB-2003 (first entry)

XX DE Maize CKI_B.

XX KW Maize; cyclin-dependent kinase inhibitor; CKI; CKI_B; plant; corn;

KW crop yield; root size; plant growth; tassel size; ear size;

KW male sterility; endoreduplication.

XX OS Zea mays.

XX PH Location/Qualifiers

PT 1..7

FT /note= "Conserved domain"

XX PN WO200281623-A2.

XX PD 17-OCT-2002.

XX PR 06-NOV-2001; 2001WO-US044038.

XX PR 07-NOV-2000; 2000US-0246349P.

XX PA (PION) PIONEER HI-BRED INT INC.

XX (ARIZ) ARIZONA BOARD OF REGENTS.

XX FI Gordon-Kamm WJ, Lowe KS, Larkins BA, Dilkes BR, Sun Y;

XX DR WPI; 2003-058511/05.

XX N-PSDB; AB74603.

PR Novel cyclin-dependent kinase polynucleotides and their encoded proteins,
 PR involved in cell cycle regulation, and useful for altering cell cycle
 PR protein content, cell cycle progression, cell number and composition of
 PR plants.

XX PS Claim 12; Page 65-66; 69pp; English.

XX The present sequence is maize cyclin-dependent kinase inhibitor (CKI),
 CC CKI_B. The coding sequence for this protein (1) is useful for modulating
 CC the activity of cyclin-dependent kinase kinase (CDK) in a plant such as a corn,
 CC soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice,
 CC barley, oil-seed Brassica and millet. Modulating the activity of CDK,
 CC preferably modulating downward is useful for providing differential
 CC growth in a plant, especially a positive growth advantage and modulating
 CC CDK activity upward is useful for increasing crop yield, root size, plant
 CC growth, tassel size and/or ear size. Modulating CDK activity is also
 CC useful for conferring male sterility and for improving transformation
 CC frequencies by increasing the number of cells in cell division. CDK
 CC activity can also be modulated for modulating endoreduplication in the

CC endosperm of corn, sorghum, wheat, rice, barley, and millet, where the
 CC promoter used is an endosperm-preferred promoter. The cell numbers are
 CC modulated in one or more tissues of a plant, comprising root, seed,
 CC tassel, ear, silk, stalk, embryo, flower, grain, germ head, leaves,
 CC stem, seed, trunk, meristem or fruit. The cells are nucleus, endosperm,
 CC pericarp, meristematic or leaf cells. (1) is also useful for identifying
 maize CKI interacting proteins, by adducting the nucleic acid sequence to
 a second nucleic acid sequence encoding a DNA-binding domain

XX SQ

Sequence 256 AA;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

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Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

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Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

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DB 6;

Length 256;

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Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

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Query Match 94.7%;

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Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

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DB 6;

Length 256;

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Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

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Query Match 94.7%;

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Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

DB 6;

Length 256;

XX

Query Match 94.7%;

Best Local Similarity 75.0%;

Matches 6;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

Score 36;

	Matches	6 ;	Conservative	0 ;	Mismatches	2 ;	Indels	0 ;	Gaps	0 ;
Qy	1	FXXXYNFD	8							
Db	233	FAAKYNF	240							

Search completed: October 26, 2004, 15:36:51
Job time : 45.6154 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode1

Run on: October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds

(without alignments)
 40.099 Million cell updates/sec

Title: US-09-574-735C-34

Perfect score: 38

Sequence: 1 FXXKYNFD 8

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters:

478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
 Listing First 45 summaries

Database : Issued Patents AA:
 1: /cgm2_6/prodata/1/iaa/5A_COMB.pep:
 2: /cgm2_6/prodata/1/iaa/5B_COMB.pep:
 3: /cgm2_6/prodata/1/iaa/6A_COMB.pep:
 4: /cgm2_6/prodata/1/iaa/6B_COMB.pep:
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 6: /cgm2_6/prodata/1/iaa/backfile1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	34	89.5	222	4	US-09-526-597D-4	Sequence 4, Appli
2	34	89.5	223	4	US-09-546-597D-6	Sequence 6, Appli
3	31	81.6	118	4	US-09-548-796A-18335	Sequence 16581, A
4	31	81.6	385	4	US-09-548-796A-16581	Sequence 536, App
5	31	81.6	648	4	US-09-538-052-536	Sequence 42, App
6	31	81.6	814	1	US-08-38A-42	Sequence 61052, A
7	30	78.9	85	4	US-09-200-767-61052	Sequence 32252, A
8	30	78.9	147	4	US-09-270-767-32252	Sequence 47469, A
9	30	78.9	147	4	US-09-546-466-2	Sequence 34019, A
10	30	78.9	170	4	US-09-270-767-34019	Sequence 49236, A
11	30	78.9	170	4	US-09-270-767-49236	Sequence 2, Appli
12	30	78.9	170	4	US-09-456-597D-2	Sequence 7509, Ap
13	30	78.9	348	4	US-09-338-352-7509	Sequence 45541, A
14	30	78.9	363	4	US-09-270-767-45543	Sequence 2, Appli
15	30	78.9	410	3	US-19-200-466-2	Sequence 30481, A
16	30	78.9	682	4	US-09-232-991A-30482	Sequence 5, Appli
17	30	78.9	1835	3	US-09-404-650-5	Sequence 2, Appli
18	30	78.9	1835	4	US-09-435-541-5	Sequence 2, Appli
19	30	78.9	1912	4	US-09-435-714C-2	Sequence 2, Appli
20	30	78.9	1968	1	US-07-45-205A-7	Sequence 45, Appli
21	30	78.9	1968	1	US-08-455-543A-45	Sequence 45, Appli
22	30	78.9	1968	2	US-08-23-305C-45	Sequence 7, Appli
23	30	78.9	1968	2	US-08-311-363-7	Sequence 4, Appli
24	30	78.9	1977	4	US-09-435-714C-4	Sequence 6, Appli
25	30	78.9	1985	4	US-09-435-714C-6	Sequence 2, Appli
26	30	78.9	2161	1	US-08-735-205A-2	Sequence 49, Appli
27	30	78.9	2161	1	US-08-455-543A-6	Sequence 49, Appli

ALIGNMENTS

RESULT 1							
US-09-526-597D-4							
;	Sequence 4, Application US/09526597D	;	Patent No. 6710227	;	GENERAL INFORMATION:	;	
;	;	;	;	;	APPLICANT: De Veylder, Lieven	;	
;	;	;	;	;	APPLICANT: Landrieu, Isabelle	;	
;	;	;	;	;	TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof	;	
;	;	;	;	;	FILE REFERENCE: 1187-2	;	
;	;	;	;	;	CURRENT APPLICATION NUMBER: US/09/526,597D	;	
;	;	;	;	;	CURRENT FILING DATE: 2000-03-16	;	
;	;	;	;	;	NUMBER OF SEQ ID NOS: 35	;	
;	;	;	;	;	SOFTWARE: PatentIn version 3.0	;	
;	;	;	;	;	SEQ ID NO: 4	;	
;	;	;	;	;	LENGTH: 222	;	
;	;	;	;	;	TYPE: PRT	;	
;	;	;	;	;	ORGANISM: Arabidopsis thaliana	;	
;	;	;	;	;	US-09-526-597D-4	;	
;	;	;	;	;	Query Match	89.5%	Score 34; DB 4; Length 222;
;	;	;	;	;	Best Local Similarity	75.0%	Pred. No. 9 2; Mismatches 2; Indexes 0; Gaps 0;
;	;	;	;	;	Matches 6; Conservative	0;	
;	;	;	;	;	;	;	
;	;	;	;	;	Qy	1 FXXKYNFD 8	
;	;	;	;	;	Db	197 FXXKYNFD 204	
RESULT 2							
US-09-526-597D-6							
;	;	;	;	;	Sequence 6, Application US/09526597D	;	
;	;	;	;	;	Patent No. 6710227	;	
;	;	;	;	;	GENERAL INFORMATION:	;	
;	;	;	;	;	APPLICANT: De Veylder, Lieven	;	
;	;	;	;	;	APPLICANT: Landrieu, Isabelle	;	
;	;	;	;	;	TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof	;	
;	;	;	;	;	FILE REFERENCE: 1187-2	;	
;	;	;	;	;	CURRENT APPLICATION NUMBER: US/09/526,597D	;	
;	;	;	;	;	CURRENT FILING DATE: 2000-03-16	;	
;	;	;	;	;	NUMBER OF SEQ ID NOS: 35	;	
;	;	;	;	;	SOFTWARE: PatentIn version 3.0	;	
;	;	;	;	;	SEQ ID NO: 6	;	
;	;	;	;	;	LENGTH: 223	;	
;	;	;	;	;	TYPE: PRT	;	
;	;	;	;	;	ORGANISM: Arabidopsis thaliana	;	
;	;	;	;	;	US-09-526-597D-6	;	
;	;	;	;	;	Query Match	89.5%	Score 34; DB 4; Length 223;

Best Local Similarity 75.0%; Pred. No. 9.2;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 FXXKYNFD 8
Db 198 FMEKYNFD 205

RESULT 3
US-09-248-796A-18335
; Sequence 18335, Application US/09248796A
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18335
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18335

Query Match Score 81.6%; DB 4; Length 118;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 FXXKYNFD 8
Db 34 FLSKENFD 41

RESULT 4
US-09-248-796A-16581
; Sequence 16581, Application US/09248796A
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16581
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16581

Query Match Score 81.6%; DB 4; Length 385;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 FXXKYNFD 8
Db 106 FNDKYNFD 113

RESULT 5
US-09-538-092-536
; Sequence 536, Application US/09538092

; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; ADDRESS: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15166-442
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SEQ ID NO 536
; SOFTWARE: CurapartSeqFormatter Version 0.9
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number YLR098C
US-09-538-092-536

Query Match Score 81.6%; Score 31; DB 4; Length 648;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8
Db 620 FALEYNFD 627

RESULT 6
US-09-233-788A-42
; Sequence 42, Application US/08233788A
; Patent No. 5635617
; GENERAL INFORMATION:
; APPLICANT: Doran, James L.
; APPLICANT: Kay, William W.
; APPLICANT: Collinson, Karen S.
; APPLICANT: Clouthier, Sharon C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
; NUMBER OF SEQUENCES: 61
; TITLE OF INVENTION: OF SALMONELLA
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/233,788A
; APPLICATION NUMBER: US/08/233,788A
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 920043.403C2
; TELEPHONE: (206) 622-4900
; TELEX: (206) 682-6131
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 814 amino acids
; TYPE: amino acid
; ;

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; TOPLOGY: linear
; MOLECULE TYPE: protein
US-08-233-788A-42

Query Match      81.6%;  Score 31;  DB 1;  Length 814;
Best Local Similarity   62.5%; Pred. No. 1.5e+02;
Matches 5;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;
SEQ ID NO: 32252
LENGTH: 147
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-47469

RESULT 7
US-09-270-767-61052
; Sequence 61052, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 61052
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-61052

Query Match      78.9%;  Score 30;  DB 4;  Length 85;
Best Local Similarity   100.0%; Pred. No. 23;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
SEQ ID NO: 34019
LENGTH: 170
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-34019

RESULT 8
US-09-270-767-32252
; Sequence 32252, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 32252
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32252

Query Match      78.9%;  Score 30;  DB 4;  Length 147;
Best Local Similarity   100.0%; Pred. No. 41;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
SEQ ID NO: 49236
LENGTH: 170
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-49236

RESULT 9
US-09-270-767-47469
; Sequence 47469, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 49236
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49236

Query Match      78.9%;  Score 30;  DB 4;  Length 170;
Best Local Similarity   100.0%; Pred. No. 48;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
SEQ ID NO: 49236
LENGTH: 170
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-49236

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 45543
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-45543

RESULT 12
Qy      4 KYNFD 8
Db      103 KYNFD 107

GENERAL INFORMATION:
Patent No.: 6710227
Aplicant: De Veylder, Lieven
Aplicant: De Almeida, Janice
Aplicant: Landrieu, Isabelle
Title of Invention: Cyclin-dependent kinase inhibitors and uses thereof
Current Application Number: US/09/526,597D
Current Filing Date: 2000-03-16
Number of SEQ ID NOS: 35
Software: PatentIn version 3.0
SEQ ID NO: 2
LENGTH: 209
TYPE: PRT
Organism: Arabidopsis thaliana
US-09-526-597D-2

Query Match    78.9%;  Score 30;  DB 4;  Length 363;
Best Local Similarity 100.0%;  Pred. No. 1e+02;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      4 KYNFD 8
Db      283 KYNFD 287

RESULT 15
US-09-140-466-2
; Sequence 2, Application US/09140466
; Patent No.: 6288160
; GENERAL INFORMATION:
; APPLICANT: CLOUGH, BARBARA
; APPLICANT: PREISER, PETER
; APPLICANT: WILSON, ROBERT
; TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
; TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHETIC INHIBITORS
; TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
; FILE REFERENCE: N68837B GWC PJC DP
; CURRENT APPLICATION NUMBER: US/09/140,466
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/056,246
; EARLIER FILING DATE: 1997-08-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
; US-09-140-466-2

Query Match    78.9%;  Score 30;  DB 3;  Length 410;
Best Local Similarity 100.0%;  Pred. No. 1.2e+02;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      4 KYNFD 8
Db      160 KYNFD 164

Search completed: October 26, 2004, 15:34:19
Job time : 14.2308 secs

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RESULT 13
US-09-328-352-7509
Sequence 7509, Application US/09328352
Patent No.: 6562958
GENERAL INFORMATION:
Aplicant: Gary L. Breton et al.
Title of Invention: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
Title of Invention: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
File Reference: GTC99-03PA
Current Application Number: US/09/328,352
Current Filing Date: 1999-06-04
Number of SEQ ID NOS: 8252
SEQ ID NO: 7509
Length: 348
TYPE: PRT
Organism: Acinetobacter baumannii
US-09-328-352-7509

Query Match    78.9%;  Score 30;  DB 4;  Length 348;
Best Local Similarity 100.0%;  Pred. No. 1e+02;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      4 KYNFD 8
Db      95 KYNFD 99

```

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RESULT 14
US-09-270-767-45543
; Sequence 45543, Application US/09270767
; Patent No.: 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

Query Match    78.9%;  Score 30;  DB 4;  Length 348;
Best Local Similarity 100.0%;  Pred. No. 1e+02;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      4 KYNFD 8
Db      95 KYNFD 99

```


Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 FXXXNFD 8 Db 228 FAKYNFD 235

RESULT 6
US-10-333-006-10
; Sequence 10, Application US/10333006
; Publication No. US2004019926A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-No. US20040019926A11le S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: INZ, Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 11887-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; PRIORITY APPLICATION NUMBER: PCT/1501/01492
; PRIORITY FILING DATE: 2003-01-14
; PRIORITY FILING DATE: 2001-06-29
; PRIORITY FILING DATE: 2000-07-14
; PRIORITY FILING DATE: 2000-07-14
; PRIORITY APPLICATION NUMBER: US 60/218,471
; PRIORITY FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 10
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-333-006-10

Query Match 94.7%; Score 36; DB 15; Length 262;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 FXXXNFD 8 Db 233 FAKYNFD 240

RESULT 7
US-10-425-114-63204
; Sequence 63204, Application US/10425114
; Publication No. US20040034880A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO: 63204
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17355F05_FLI.pep

Query Match 94.7%; Score 36; DB 15; Length 263;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 FXXXNFD 8 Db 235 FAKYNFD 242

RESULT 8
US-10-437-963-122432
; Sequence 122432, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Babazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 122432
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2535C.1.pep
US-10-437-963-122432

Query Match 94.7%; Score 36; DB 16; Length 354;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 FXXXNFD 8 Db 219 FAKYNFD 226

RESULT 9
US-10-437-963-195115
; Sequence 195115, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Babazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 195115
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91095C.1.pep
US-10-437-963-195115

Query Match 94.7%; Score 36; DB 16; Length 417;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 1 FXXXKYNF 8
Db 388 FAAKYNEF 395

RESULT 10
US-10-437-963-122443
Sequence 122443, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 122443
LENGTH: 423
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_2536C.1.pep

RESULT 11
US-10-437-963-122443
Query Match 94.7%; Score 36; DB 16; Length 423;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 FXXXKYNF 8
Db 232 FAAKYNEF 239

RESULT 11-13
US-10-437-963-122443
Sequence 122443, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 212181
LENGTH: 176
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_33625C.1.pep

RESULT 12
US-09-733-507-16
Sequence 16, Application US/09733507
Patent No. US2001005379A1
GENERAL INFORMATION:
APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
FILE REFERENCE: 81601.2
CURRENT APPLICATION NUMBER: US/09/733,507
PRIORITY APPLICATION NUMBER: CA 2,256,121
PRIOR FILING DATE: 1998-12-31
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 196
TYPE: PRT
ORGANISM: Chenopodium rubrum
US-09-733-507-16

Query Match 92.1%; Score 35; DB 9; Length 196;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXXKYNF 8
Db 171 FSEKYNED 178

RESULT 13
US-10-451-139-15
Sequence 15, Application US/10451139
Publication No. US20040098763A1
GENERAL INFORMATION:
APPLICANT: WANG, HONG
APPLICANT: ZHOU, YONGMING
APPLICANT: FOWKE, LARRY C.
APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
AGRICULTURE AND AGRIFOOD CANADA
TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
FILE REFERENCE: 4810-62237
CURRENT APPLICATION NUMBER: US/10/451,139
PRIORITY APPLICATION NUMBER: NO PCT/CA01/01825
PRIOR FILING DATE: 2001-12-18
PRIORITY APPLICATION NUMBER: US 60/255,908
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 196
TYPE: PRT
ORGANISM: Chenopodium rubrum
US-10-451-139-15

Query Match 92.1%; Score 35; DB 15; Length 196;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXXKYNF 8
Db 171 FSEKYNED 178

RESULT 14
US-10-011-588-31
Sequence 31, Application US/10011588
Publication No. US2002016877A1
GENERAL INFORMATION:
APPLICANT: Smith, Leonard
APPLICANT: Jensen, Melody

RESULT 15
US-10-011-588-11
; Sequence 11, Application US/10011588
; Publication No. US20020168727A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Leonard
; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN RESEARCH AND CLINICAL THERAPY
; TITLE OF INVENTION:
; FILE REFERENCE: A34796 067252.0113
; CURRENT APPLICATION NUMBER: US/10/011,588
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/910,186
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/246,744
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 60/311,966
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 31
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Protein encoded by SEQ ID NO:30
US-10-011-588-31

Query Match	92.1%	Score 35;	DB 13;	Length 440;
Best Local Similarity	75.0% ;	Pred. No. 69;		
Matches	6;	Conservative	0;	Mismatches
			2;	Indels
			0;	Gaps
			0;	

Qy 1 FXXKYNFD 8
Db 324 FSEKYNFD 331

RESULT 15
US-10-011-588-11
; Sequence 11, Application US/10011588
; Publication No. US20020168727A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, Leonard
; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN RESEARCH AND CLINICAL THERAPY
; TITLE OF INVENTION:
; FILE REFERENCE: A34796 067252.0113
; CURRENT APPLICATION NUMBER: US/10/011,588
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/910,186
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/246,744
; PRIOR FILING DATE: 2000-11-06
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic botulinum neurotoxin light chain of
; OTHER INFORMATION: serotype D based on wild-type Clostridium
; OTHER INFORMATION: botulinum sequence
US-10-011-588-11

Query Match	92.1%	Score 35;	DB 13;	Length 441;
Best Local Similarity	75.0% ;	Pred. No. 69;		
Matches	6;	Conservative	0;	Mismatches
			2;	Indels
			0;	Gaps
			0;	

Qy 1 FXXKYNFD 8
Db 325 FSEKYNFD 332



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:13 ; Search time 11.0769 Seconds
(without alignments)
69.490 Million cell updates/sec

Title: US-09-574-735C-34

Perfect score: 38

Sequence: 1 FXKKNFD 8

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing First 45 summaries

Database : PIR_79;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	92.1	196	T09968	cyclin-dependent kinase inhibitor protein (PAS and AAA domains) [imported] - Clostridium acetobutylicum
2	35	92.1	627	D96956	ntrC family transactivator
3	35	92.1	1276	S11455	botulinum neurotoxin
4	35	92.1	1285	S70582	botulinum neurotoxin
5	35	92.1	1664	S67250	DNA-directed RNA polymerase
6	34	89.5	191	T01132	cyclin-dependent kinase inhibitor (EC 3.2.19.1)
7	34	89.5	699	A38368	chitinase (EC 3.2.19.1)
8	34	89.5	1635	T14075	hypothetical proteolipid-like protein
9	32	84.2	195	H96532	lectin-like protein
10	31	81.6	272	S71252	very late factor 1
11	31	81.6	374	T10349	hypothetical proteolipid-like protein
12	31	81.6	480	T08866	probable cycl-CoA
13	31	81.6	603	G84554	transcription activator
14	31	81.6	648	S39723	fimbrial outer membrane
15	31	81.6	814	C40618	outer membrane film
16	31	81.6	838	AC1064	hypothetical protein
17	31	81.6	1050	H90316	hypothetical protein
18	30	78.9	114	AC3246	hypothetical protein
19	30	78.9	149	A70325	hypothetical protein
20	30	78.9	209	T46140	hypothetical protein
21	30	78.9	232	F64576	hypothetical protein
22	30	78.9	251	T40710	hypothetical protein
23	30	78.9	260	D64119	hypothetical protein
24	30	78.9	265	T22973	hypothetical protein
25	30	78.9	286	B99546	sulfite adenyllyltransferase
26	30	78.9	302	B84979	flagellar motor subunit
27	30	78.9	315	H84938	heptaprenyl diphosphatase
28	30	78.9	321	AB1316	heptaprenyl diphosphatase
29	30	78.9	321	AB1688	heptaprenyl diphosphatase

RESULT 1

T09968

cyclin-dependent kinase inhibitor protein - red goosefoot

C;Species: *Chenopodium rubrum* (red goosefoot)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T09968

R;Pountain, M.D.; Renz, A.; Beck, E.

submitted to the EMBL Data Library, November 1997

A;Description: A Plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic

A;Reference number: Z16910

A;Accession: T09968

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-196 <FOUR>

A;Cross references: UNIPROT:O48597; EMBL:AJ002173

A;Experimental source: photoautotrophic cells derived from hypocotyl tissue

A;Genetics:

A;Gene: CDK11

C;Keywords: protein kinase inhibitor

ALIGNMENTS

Query	Match	Score	Local Similarity	DB 2;	Length	196;
Matches 6; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;		
Qy 1 FXXKYNFD 8	Db 171 FSEKYNFD 178					

RESULT 2

D96956

ntrC family transcription regulator (PAS and AAA domains) [imported] - Clostridium acetobutylicum

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: D96956

R;Nolling, J.; Breson, G.; Omelichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, C.; Koonin, E.V.; Smith, D.R.

J; Bacteriol. 183: 4833-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-producing Bacterium *C*.

A;Accession: D96956

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-627 <KUR>

A;Cross references: UNIPROT:Q97UJ5; GB:AE001471

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC0459

Query	Match	Score	Local Similarity	DB 2;	Length	627;
Matches 6; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;		

Wednesday Oct 27 09:35:38 2004

Query Match 89.5%; Score 34; DB 2; Length 191;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
Db 167 FKKKYNFD 174

RESULT 7
A38168 chitinase (EC 3.2.1.14) Precursor - *Bacillus circulans*
C;Species: *Bacillus circulans*
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 09-Jul-2004
C;Accession: A38168
R;Matanabe, T.; Suzuki, K.; Oyanagi, W.; Ohnishi, K.; Tanaka, H.,
J. Biol. Chem. 265, 15559-15655, 1990
A;Title: Gene cloning of chitinase A1 from *Bacillus circulans* WL-12 revealed its evolution
A;Reference number: A38368; MUID:90368776; PMID:2203782
A;Accession: A38368
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-699 <WAT>
A;Cross-references: UNIPROT:P20533; GB:M57601; GB:J05599; NID:91066341; PIDN:AAA81528.1;
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 89.5%; Score 34; DB 2; Length 699;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
Db 190 FLRKYNFD 197

RESULT 8
T14075 chitinase (EC 3.2.1.14) - yellow fever mosquito
C;Species: *Aedes aegypti* (yellow fever mosquito)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14075
R;de la Vega, H.; Specht, C.A.; Liu, Y.; Robbins, P.W.,
Insect Mol. Biol. 7, 233-239, 1997
A;Title: Chitinases are a multi-gene family in *Aedes*, *Anopheles*, and *Drosophila*.
A;Reference number: Z17872
A;Accession: T14075
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1635
A;Cross-references: UNIPROT:O17412; EMBL:AF026492; NID:92564720; PIDN:AABB
C;Genetics:
A;Gene: CRM2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: Glycosidase; hydrolase; polysaccharide degradation

Query Match 89.5%; Score 34; DB 2; Length 1635;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
Db 1365 FIEKYNYFD 1372

RESULT 9
H96532 hypothetical protein F14J22.14 [imposted] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: H96532
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspil, N.A.; Kaul, S.; White, O.; Alonso, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conn, R.; Creasy, T.H.; Dewart, K.; Rohrman, G.F.

Query Match 81.6%; Score 31; DB 2; Length 374;
Best Local Similarity 62.5%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
Db 170 FTEKYNFD 177

RESULT 10
S71252 lectin-like protein - *Arabidopsis thaliana* (mouse-ear cress)
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S71252
R;Herve, C.; Lescure, B.,
submitted to the EMBL Data Library, September 1995
A;Description: An *Arabidopsis thaliana* cDNA encoding a lectin like protein.
A;Reference number: S71252
A;Accession: S71252
A;Molecule type: mRNA
A;Residues: 1-272
A;Cross-references: UNIPROT:Q39205; EMBL:X91259; NID:9995618; PID:9995619
C;Superfamily: plant lectin
C;Keywords: lectin

Query Match 81.6%; Score 31; DB 2; Length 272;
Best Local Similarity 62.5%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
Db 18 FAVKFNFD 25

RESULT 11
T10349 very-late factor 1 protein - *Oryza pseudosugata* nuclear polyhedrosis virus
C;Species: *Oryza pseudosugata* nuclear polyhedrosis virus, OPNNPV
C;Accession: T10349
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrman, G.F.,
Virology 229, 381-399, 1997
A;Title: The sequence of the *Oryza pseudosugata* multinucleocapsid nuclear polyhedros.
A;Reference number: Z17011; MUII:9721300; PMID:9126251
A;Accession: T10349
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-374 <AHR>

Query Match 81.6%; Score 31; DB 2; Length 374;
Best Local Similarity 62.5%; Pred. No. 54;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FXXXYNFD 8
Db 1911326 AAC59079.1; PIDN: AAC59079.1; PID:911326

Qy 1 FXXXYNFD 8
 Db 335 YLNKYNFD 342

RESULT 12
 T08866 hypothetical protein A_TM017A05.12 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 11-Jun-1999 #sequence_change 09-Jul-2004
 C;Accession: T08866
 R;Waterson, N.
 submitted to the EMBL Data Library, October 1997
 A;Reference number: 216500
 A;Accession: T08866
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q9SEY5; EMBL:AF024504; NID:g2435510; PMID:g2435522; GSPDB:GN0
 A;Experimental source: cultivar Columbia
 C;Genetics:
 A;Gene: ATSP; A_TM017A05.12
 A;Map Position: 4
 C;Superfamily: probable acyl-CoA ligase homology <ACL>
 P;7-4/70/Domain: acetate-CoA ligase homology

Query Match Best Local Similarity 81.6%; Score 31; DB 2; Length 480;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXXYNFD 8
 Db 88 FASKYSFD 95

RESULT 13
 G84554 probable acyl-CoA synthetase [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: G84554
 C;Accession: G84554
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 Euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.;
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A844200; PMID:20083487; PMID:10617197
 A;Accession: G84554
 A;Molecule type: DNA
 A;Residues: 1-603 <STOP>
 A;Cross-references: UNIPROT:Q9SEY5; GB:AE002093; NID:96598797; PMID:AAF18674.1; GSPDB:GN
 C;Genetics:
 A;Gene: At2g17650
 A;Map position: 2
 C;Superfamily: probable acyl-CoA ligase medium chain; acetate-CoA ligase homology

Query Match Best Local Similarity 81.6%; Score 31; DB 2; Length 603;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXXYNFD 8
 Db 211 FASKYSFD 218

RESULT 14
 S55723 transcription activator CHA4 - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein L2552; protein YLR098C
 C;Species: Saccharomyces cerevisiae
 C;Accession: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
 C;Accession: S55723; S64932; S72236

Qy 1 FXXXYNFD 8
 Db 21 FSRQYNFD 28

Search completed: October 26, 2004, 15:40:06
 Job time : 14.0769 secs



GenCore version 5.1.6
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CM protein - Protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 44.6154 Seconds
 {without alignments}
 103.171 Million Cell updates/sec

Title: US-09-574-735C-34
 Perfect score: 38
 Sequence: 1 PXXKYNFD 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02:
 1: uniprot_sprot:
 2: uniprot_trembl:
 * * *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	3.6	Q6Z6G5	Q6Z6G5	262	2 BADI7213	0626G5 oryza sativ
2	3.6	Q6Z6G5	Q6Z6G5	262	2 C17419	017419 anopheles s
3	3.5	Q6Z6G5	Q6Z6G5	113	2 O45597	048597 chenopodium
4	3.5	Q6Z6G5	Q6Z6G5	196	2 Q8GU2	Q8GU2 nicotiana t
5	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q8EV36	Q8EV36 mycoplasma
6	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q9TJU5	Q9TJU5 clostridium
7	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q9TQG7	Q9TQG7 clostridium
8	3.5	Q6Z6G5	Q6Z6G5	92.1	2 BXD_CLOBO	P19321 clostridium
9	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q45967	Q45967 clostridium
10	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q9LBR1	Q9LBR1 clostridium
11	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q9LRA3	Q759A3 ashbya goss
12	3.5	Q6Z6G5	Q6Z6G5	92.1	2 QAS52294	Aas52294 ashbya go
13	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q6FV16	Q6FV16 candida gla
14	3.5	Q6Z6G5	Q6Z6G5	92.1	2 Q6CIX4	Q6CIX4 kluveromyces
15	3.5	Q6Z6G5	Q6Z6G5	92.1	1 RPA1 YEAST	P10964 saccharomyces
16	3.5	Q6Z6G5	Q6Z6G5	92.1	1 RPA1 YEAST	O17414 anopheles s
17	3.4	Q6Z6G5	Q6Z6G5	89.5	2 O17414	Q93YF6 nicotiana t
18	3.4	Q6Z6G5	Q6Z6G5	89.5	2 O93YF6	Q93YF6 nicotiana t
19	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q93YF6	Q93YF6 nicotiana t
20	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q93YF6	Q93YF6 lycopersico
21	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q93YF6	Q93YF6 arabidopsis
22	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q93YF6	Q93YF6 arabidopsis
23	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q93YF6	Q93YF6 arabidopsis
24	3.4	Q6Z6G5	Q6Z6G5	89.5	1 Q8LDX1	Q8LDX1 arabidopsis
25	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q9LRL5	Q9LRL5 arabidopsis
26	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q8GT29	Q8GT29 lycopersico
27	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q9FXB5	Q9FXB5 arabidopsis
28	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q7XDR8	Q7XDR8 oryza sativ
29	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q9FM65	Q9FM65 oryza sativ
30	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q8GXJ3	Q8GXJ3 arabidopsis
31	3.4	Q6Z6G5	Q6Z6G5	89.5	2 Q94C90	Q94C90 arabidopsis

ALIGNMENTS

RESULT 1									
ID	Q6Z6G5	PRELIMINARY;	PRT;	262 AA.					
AC	Q6Z6G5;				AC	TREMBL1; 27, Created)			
DT	05-JUL-2004	(TREMBL1; 27, Last sequence update)			DT	05-JUL-2004	(TREMBL1; 27, Last annotation update)		
DT	05-JUL-2004	(TREMBL1; 27, Last sequence update)			DT	05-JUL-2004	(TREMBL1; 27, Last annotation update)		
DE	Hypothetical protein P0486G03.18;				DE	Hypothetical protein P0486G03.18;			
GN	Orzva sativa (japonica cultivar-group).				GN	Orzva sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;				OC	Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;			
NCBI_TaxID	39947;				NCBI_TaxID	39947;			
RN	[1]				RN	[1]			
RP	SEQUENCE FROM N.A.				RP	SEQUENCE FROM N.A.			
RA	Sasaki T., Matsumoto T., Yamamoto K.;				RA	Sasaki T., Matsumoto T., Yamamoto K.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
EMBL	AB05002; BAD17213.1;				EMBL	AB05002; BAD17213.1;			
DR	InterPro: IPR003175; CDI.				DR	InterPro: IPR003175; CDI.			
DR	PFam: PF02234; CDI; 1.				DR	PFam: PF02234; CDI; 1.			
KW	Hypothetical protein				KW	Hypothetical protein			
SEQUENCE	262 AA;				SEQUENCE	262 AA;			
QY	1 FXXXYNFD 8				QY	1 FXXXYNFD 8			
Score	94.7%				Score	94.7%			
Match	36				Match	36			
Best Local Similarity	75.0%				Best Local Similarity	75.0%			
Matches	6				Matches	6			
Conservative	0;				Conservative	0;			
Indels	2;				Indels	2;			
Gaps	0;				Gaps	0;			
Db	233 FAAXYNFD 240				Db	233 FAAXYNFD 240			

SEQUENCE FROM N.A.

STRAIN=CV.

Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;

OC

Spermatozoa; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC

Ehrhartoideae; Orzeae; Oryza; Oryza sativa.

OC

NCBI_TaxID=39947;

RN

SEQUENCE FROM N.A.

STRAIN=CV.

Sasaki T., Matsumoto T., Yamamoto K.;

RA

"Oryza sativa nipponbare (GA3)" Genomic DNA, chromosome 2, PAC

RT

clone P0486G03.18;

RT

Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RI

DR EMBL; AP005002; BAD17213_1; -
 KW Hypothetical Protein
 SEQUENCE 262 AA; 27138 MW; 42ECB5C8276C0726 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 262;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FXXKYNFD 8
 Db 233 FAARYNFD 240

RESULT 3
 ID O17419 PRELIMINARY; PRT; 113 AA.
 AC O17419_05_Created
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Chitinase (Fragment).
 GN Anopheles stephensi (Indo-Pakistan malaria mosquito).
 OC Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles
 OC NCBI_TaxID:30069;, RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98324849; PubMed=9662472;
 RA de la Vega H., Specht C.A., Liu Y., Robbins P.W.;
 RT "Chitinases are a multi-gene family in Aedes, Anopheles and
 Drosophila.";
 RL Insect Mol Biol. 7:233-239 (1998).
 DR AF26499; AMB:8857.1; -.
 RSSP: QI3231; LG22.
 DR GO: GO:0006787; F:hydrolyase activity; IEA.
 DR InterPro: IPR001223; Glyco_hydro_18AS.
 DR Pfam: PF00704; Glyco_hydro_18_1.
 DR PROSITE: PS01055; CHITINASE_18; PARTIAL.
 FT NON_TER 1 113
 SQ SEQUENCE 113 AA; 13188 MW; 5EA7DCAB54B4B97 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 113;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FXXKYNFD 8
 Db 100 FAAYNFD 107

RESULT 4
 ID O48597 PRELIMINARY; PRT; 196 AA.
 AC O48597_05_Created
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cyclin-dependent kinase inhibitor protein.
 GN Chenopodium rubrum (Red goosefoot) (pigweed).
 OC Spermatophytina; Magnoliophyta; Embryophytina; Tracheophytina;
 OC Caryophyllales; Amaranthaceae; Chenopodiaceae.
 OC NCBITaxID=3550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9332903; PubMed=10409053;
 RA Fountain M.D., Renz A., Beck E.;
 RT "Isolation of a cDNA encoding a G1-cyclin-dependent kinase inhibitor

RT from suspension-cultured photoautotrophic chenopodium rubrum cells.";
 RL Plant Physiol. 120:339-339 (1999).
 DR EMBL; AU002173; CAA05215_1; -.
 DR PIR; T09968; T09968.
 GO; GO:000534; C:nucleus; IEA.
 DR GO; GO:004861; F:cyclin-dependent protein kinase inhibitor a...; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR InterPro; IPR03175; CDI.
 DR PF02234; CDI; 1.
 KW Cyclin; Kinase.

SQ SEQUENCE 196 AA; 21685 MW; 150349F7BD82A6B2 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 196;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8
 Db 171 FSBKYNFD 178

RESULT 5
 ID Q8GUAA2 PRELIMINARY; PRT; 207 AA.
 AC Q8GUAA2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Cyclin-dependent kinase inhibitor protein.
 GN Name=K152;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Stramenoplyta; Embryophytina; Tracheophytina;
 OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RN SEQUENCE FROM N.A.
 RA Jasinski S., Saraiava Leite C., Domenichini S., Stevens R., Raynaud C.,
 RA Perennes C., Bergounioux C., Glab N.;
 RA "NTK152, a novel tobacco cyclin-dependent kinase inhibitor
 differentially expressed during the cell cycle and plant
 development.";
 RL Plant Physiol. Biochem. 41:667-676 (2003).
 DR EMBL; AJ517189; CAD56868_1;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a...; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR InterPro; IPR03175; CDI.
 DR PF02234; CDI; 1.
 KW Cyclin; Kinase.

SQ SEQUENCE 207 AA; 23278 MW; F5AE70AD2261BC2D CRC64;

Query Match 92.1%; Score 35; DB 2; Length 207;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FXXKYNFD 8
 Db 180 FTAKYNFD 187

RESULT 6
 ID Q8EV36 PRELIMINARY; PRT; 442 AA.
 AC Q8EV36;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Conserved hypothetical.
 GN OrderedLocusMamm-MPE7310;
 OS Mycoplasma penetrans.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NCBITaxID=28227;
 RN SEQUENCE FROM N.A.
 STRAIN=HF2;
 MEDLINE=2354719; PubMed=12466555;
 Sasaki Y., Ishikawa J., Yanashita A., Oshima K., Kenri T., Furuya K.,
 Yoshino C., Horino A., Shiba T., Saeki T., Hattori M.;
 RT "The complete genomic sequence of Mycoplasma penetrans, an
 intracellular bacterial pathogen in humans.";
 RL Res. Nucleic Acids Res. 30:5293-5300(2002).
 EMBL: AP004173; BAC44525.1;
 DR Complete proteome; Hypothetical protein.
 KW Sequence 442 AA; 50767 MW;
 SEQUENCE 442 AA;

Query Match 92.1%; Score 35; DB 2; Length 442;
 Best Local Similarity 75.0%; Pred. No. 66;
 Matches 6; Conservative 0; Gaps 0;
 Indels 0; Gaps 0;

Qy 1 FXXXXNFD 8
 Db 60 FXXXXNFD 67

RESULT 7
 Q97IUS ID Q97IUS PRELIMINARY; PRT; 627 AA.
 AC 01-OCT-2001 (TREMBLrel. 1B, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE NtrC family transcriptional regulator (PAS and AAA domains).
 GN Orderadicusshames-OAC0459;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiaceae;
 OC Clostridium.
 RN [1] NCBITaxID=1488;
 RP SEQUENCE FROM N.A.
 RC STRAIN=AVCC 824 / DSM 792 / VRM B-1787;
 PX MEDLINE=21359325; PubMed=14466206;
 RX DOI=10.1128/JB.183.1823-1833.2001;
 Noelling J., Bretton G., Omelichenko M.V., Makarova K.S., Zeng Q.,
 Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 Tatusov R.L., Sabate P., Doucette-Stamm L.A., Souaille P.,
 Daly M.J., Bennett G.N., Konon E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 CC - SIMILARITY: Contains 1 sigma-S4 factor interaction ATP-binding
 domain.

DR EMBL: AB007560; AAK78439.1; -.
 DR PIR: D96356; D96916.
 GO: GO:000016; F:nucleotide binding; IEA.
 DR GO: GO:0004871; F:signal transducer activity; IEA.
 GO: GO:0000160; P:two-component signal transduction system (p. . .); IEA.
 InterPro: IPR035932; AAA_ABase.
 InterPro: IPR09057; HomeoDomain-like.
 InterPro: IPR02197; HTH_Fis.
 InterPro: IPR00014; PAS_.
 InterPro: IPR010524; PPR_N.
 InterPro: IPR02078; S194_interact.
 DR SMART; SMC0382; AAA; 1.
 SMART; SMC0919; PAS; 1.
 Pfam: PF02954; HTH_8; 1.
 Pfam: PF00989; PAS; 1.
 DR Pfam: PF06506; PPR_N; 1.
 DR SMART; SMC0158; Sigma54_activat; 1.
 SMART; SMC0919; PAS; 1.
 TIGRFAMS; TIGR01199; HTH_fis; 1.
 DR TIGRFAMS; TIGR00223; sensory_box; 1.
 PROSITE; PS50112; PAS; 1.
 DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.

DR PROSITE; PS00676; SIGMA54_INTERACT_2; 1.
 DR PROSITE; PS00455; SIGMA54_INTERACT_4; 1.
 RN AT->binding; Complete Proteome; DNA-binding; Transcription regulation.
 SEQUENCE 627 AA; 71082 MW; 4A652FAAB36; ADC CRC6;
 Query Match 92.1%; Score 35; DB 2; Length 627;
 Best Local Similarity 75.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FXXXXNFD 8
 Db 311 FXXXXNFD 318

RESULT 8
 Q9QTG7 ID Q9QTG7 PRELIMINARY; PRT; 1275 AA.
 AC 09QTG7; PRELIMINARY;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE NTX (Fragment).
 GN Name=Fnx;
 OS Clostridium botulinum D bacteriophage.
 OC Viruses.
 OX NCBI_TaxID=29342;
 RN [1] TAXID=29342;
 RP SEQUENCE FROM N.A.
 RC STRAIN=1873;
 RX MEDLINE=99017546; PubMed=9802560;
 RA Nakajima R., Inoue K., Ikeda T., Fujinaga Y., Sunagawa H., Takeshi K., Ohyama T., Watanabe T., Inoue K., Oguma K.;
 RT "Molecular composition of the 16S toxin produced by a Clostridium botulinum type D strain, 173.";
 RL Microbiol Immunol. 42:59-605(1998).
 DR EMBL: AB012112; BAA71084.1;
 DR GO: GO:0008933; P:peptidase activity; IEA.
 DR GO: GO:0009405; P:peptidogenesis; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR011591; Botulinum
 DR InterPro: IPR006308; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR011065; Kunin-like.
 DR InterPro: IPR000395; Peptidase M27.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27_1.
 DR PRINTS; PR00760; BONTOXIYNSIN.
 DR ProDom; PD001963; Botulinum_1.
 DR PROSITE; PS01042; ZINC_Protease; UNKNOWN_1.
 FT NON_TER 1275 AA; 146742 MW;
 SQ SEQUENCE 1275 AA; 146742 MW; 3C50P46CB213E2D6 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 1275;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 FXXXXNFD 8
 Db 326 FXXXXNFD 333

RESULT 9
 BX_CLOBO ID BX_CLOBO STANDARD; PRT; 1276 AA.
 AC P19321;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BotNT/D)
 DE Name=bord;
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridaceae;
 OC Clostridium.

OX		NCBI_TaxID=1491;	
RN	[1]	SEQUENCE FROM N.A.	
RC	STRAIN=Type D / BVD/-3;		
RX	MEDLINE=91016853; PubMed=2216736;		
RA	Binz T., Kurazawa H., Popoff M.R., Eklund M.W., Sakaguchi G., Kozaki S., Kriegstein K., Henschen A., Gill D.M., Niemann H., RT "Neurotoxin sequence of the gene encoding Clostridium botulinum neurotoxin type D"; Nucleic Acids Res. 18:5556-5556(1990).		
RL	[2]	SEQUENCE FROM N.A.	
RP	STRAIN=Type D / CB-16'; MEDLINE=93042276; PubMed=1420572;		
RC	Sunagawa H., Ohyama T., Watanabe T., Inoue K.; "The complete amino acid sequence of the Clostridium botulinum type D neurotoxin, deduced by nucleotide sequence analysis of the encoding phage d-16' phi genome"; J. Vet. Med. Sci. 54:905-913(1992).		
RN	[3]	PARTIAL SEQUENCE.	
RP	STRAIN=Type D / South African; PubMed=2668193; MEDLINE=89133741; PubMed=89133741;		
RC	Morishita K., Syuto B., Kubo S., Oguma K.; "Molecular diversity of neurotoxins from Clostridium botulinum type D strains"; Infect. Immun. 57:2886-2891(1989).		
RL	[4]	IDENTIFICATION OF SUBSTRATE.	
RP	MEDLINE=94230352; PubMed=8175689;		
RC	Yanasaki S., Baumeister A., Binz T., Bläsi J., Link S., Cornville F., Rogues B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.; "Cleavage of members of the synaptobrevin/VAMP family by types D and F botulinial neurotoxins and tetanus toxin.", J. Biol. Chem. 269:127164-127172(1994).		
CC	-.- FUNCTION: Botulinum toxin acts by inhibiting neurotransmitter release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that cleaves the 60-Lys- -Leu-61 bond of synaptobrevin-1 and -2.		
CC	-.- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxis. No detected action on small molecule substrates.		
CC	-.- COFACTOR: Binds 1 zinc ion per subunit (By similarity).		
CC	-.- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, formation and toxin binding, respectively.		
CC	-.- SUBCELLULAR LOCATION: Secreted.		
CC	-.- MISCELLANEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.		
CC	-.- MISCELLANEOUS: Botulinum type D neurotoxin is synthesized by strains of C botulinum which carry the appropriate bacteriophage.		
CC	-.- SIMILARITY: Belongs to peptidase family M27.		
CC	This SWISS-PROT entry is copyright. It is produced through collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).		
EMBL	X54254; CAA3815.1;		
EMBL	S49077; AAB24244.1;		
PIR	S11455; S11455.		
HSSP	P10844; 1P31.		
MEROPS	M27_0002;		
InterPro	IPIR008985; ConA_like_lec_g1.		
InterPro	IPIR01065; Peptidase_M27.		
InterPro	IPIR00625; Pept M Zn BS.		
InterPro	IPI01742; Peptidase_M27_1.		
PRINTS	PR00760; BONTOXILIN.		
ProDom	PD001963; Botulinum.		
PROSITE	PS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	Neurotoxin.		
SEQUENCE	1285 AA; 147365 MW; EBD9BEBECA6C413 CRC64;		
SQ	Query Match Score 35; DB 1; Length 1276; Best Local Similarity 92.1%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0; Matches 6; Conservative 6; Sequence 1276 AA; 146671 MW; C1EC50F46C8233E2 CRC64;	Qy 1 FXXKYNFD 8 Db 326 FSEKYNFD 333	
	RESULT 10 Q45967 PRELIMINARY: ID 045967 PRT; 1285 AA. AC 045967; DT 01-NOV-1996 (TREMBrel. 01, Created) DT 01-NOV-1996 (TREMBrel. 01, Last sequence update) DT 01-MAR-2004 (TREMBrel. 26, Last annotation update) DE Neurotoxin consisting of botulinum neurotoxin D and C1. OS Clostridium botulinum D. OC Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae; OC Clostridium. RN [1] PRT; TaxID=366829; RP SEQUENCE FROM N.A. RC STRAIN=South African; MEDLINE=962283801; PubMed=8679691; RX Moriishi K., Koura M., Abe N., Fujii N., Fujinaga Y., Inoue K., Ogumad K.; "Mosaic structures of neurotoxins produced from Clostridium botulinum types C and D organisms." RLBiochim. Biophys. Acta 1307:123-126(1996). DR HSSP; P10844; 1F31. DR MEROPS; M27_002; - DR GO; GO:0008233; P: peptidase activity, IEA. DR GO; GO:0009405; P: pathogenesis; IEA. DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA. DR InterPro; IPIR01591; Botulinum. DR InterPro; IPIR008985; ConA-like_lec_g1. DR InterPro; IPIR011065; KunitZ-like. DR InterPro; IPIR003595; Peptidase_M27. DR InterPro; IPIR00625; Pept M Zn BS. DR PRAM; PF001742; Peptidase_M27_1. DR PRINTS; PR00760; BONTOXILIN. DR ProDom; PD001963; Botulinum. DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1. KW Neurotoxin.		

Best Local Similarity 75.0%; Matches 6; Conservative 0; Mismatches 0; Gaps 0;	Pred. No. 2e+02; Indels 0; Gaps 0;	
QY 1 FXXKYNFD 8		
DB 326 FSEKYNFD 333		
RESULT 11		
Q91BRI Q91BRI PRELIMINARY; PRT; 1285 AA.		
AC DT 01-OCT-2000 (TREMBlrel. 15, Created)		
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)		
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)		
DE Neurotoxin.		
DOC Clostridium botulinum.		
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;		
Clostridium.		
NCBI TaxID=1491;		
[1]		
SEQUENCE FROM N.A.		
STRAIN=D-4947 N.A.		
MEDLINE=21659147; PubMed=11713244;		
RA Kouguchi H., Watanabe T., Segane Y., Sunagawa H., Ohyama T.;		
"in vitro" reconstitution of the Clostridium botulinum type D		
progenitor toxin."; J. Biol. Chem. 277:2650-2656 (2002).		
EMBL; AB037920; BA90661.1; -.		
HSSP; PI0844; IFA31.		
MEROPS; M27_002; -.		
DR GO; GO:0008233; F-peptidase activity; IEA.		
GO; GO:0009405; Pathogenesis; IEA.		
GO; GO:0006508; Proteinolysis and peptidolysis; IEA.		
InterPro; IPR011591; Botulinum.		
InterPro; IPR08985; ConA-like_lec_g1.		
InterPro; IPR01065; Kunitz_like.		
InterPro; IPR000395; Peptidase_M27.		
InterPro; IPR006025; Peptidase_Mn_BS.		
PFam; PF01742; Peptidase_M27_1.		
PRNTIS; PR00760; BONTOXITYSIN.		
ProDom; PD001363; Botulinum_1.		
Prosite; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
SEQUENCE 1285 AA; 147351 MW; B63AFA487D570680 CRC64;		
Query Match 92.1%; Score 35; DB 2; Length 1285;		
Best Local Similarity 75.0%; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY 1 FXXKYNFD 8		
DB 326 FSEKYNFD 333		
RESULT 12		
Q759A3 Q759A3 PRELIMINARY; PRT; 1640 AA.		
AC DT 05-JUL-2004 (TREMBlrel. 27, Created)		
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DE ADR374CP.		
Name-ADR374C.		
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).		
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;		
Saccharomycetales; Saccharomycetaceae; Bremothecium.		
NCBI TaxID=33169;		
[1]		
SEQUENCE FROM N.A.		
STRAIN=ATCC 10895;		
PubMed=15001715;		
Dierfaff F.S.; Voegelei S.; Brachat S.; Lerch A.; Gaffney T.,		
RA "The Ashbya gossypii genome as a tool for mapping the ancient		
RT Saccharomyces cerevisiae genome.",		
RT Science 304:304-307 (2004).		
RL [2]		
SEQUENCE FROM N.A.		
RC STRAIN=ATCC 10895;		
RA Voegelei S.E.; Brachat S.; Dietrich F.S.; Lerch A.; Gaffney T.,		
RA Philippson P.; Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.		
EMBL; AE016893; AAS52294.1; -.		
AGD; ADR374C; -.		
DR InterPro; IPR000345; CytC_heme_BS.		
DR InterPro; IPR006592; RNA_Pola_N.		
DR InterPro; IPR007022; RNA_Pol_A.		
DR InterPro; IPR007080; RNA_Pol_Bpb1_1.		
DR InterPro; IPR007066; RNA_Pol_Rpb1_1.		
DR InterPro; IPR007083; RNA_Pol_Rpb1_4.		
DR InterPro; IPR007081; RNA_Pol_Rpb1_5.		
DR InterPro; IPR007082; RNA_Pol_Rpb1_1.		
DR Pfam; PF006223; RNA_Pol_Rpb1_2; 1.		
DR Pfam; PF004983; RNA_Pol_Rpb1_3; 1.		
DR Pfam; PF05000; RNA_Pol_Rpb1_4; 1.		
DR Pfam; PF01998; RNA_Pol_Rpb1_5; 1.		
DR SMART; SM00663; RPOIA_N_1.		
DR PROSITE; PS00190; CRYPTOCHROME_C; UNKNOWN_1.		
SEQUENCE 1640 AA; 182887 MW;		
Query Match 92.1%; Score 35; DB 2; Length 1640;		
Best Local Similarity 75.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;		
Matches 6; Conservative 0; MisMatches 0; Indels 0; Gaps 0;		
QY 1 FXXKYNFD 8		
Db 1432 FISKYNFD 1439		
RESULT 13		
AAS52294 ID AAS52294 PRELIMINARY; PRT; 1640 AA.		
AC AAS52294; DT 23-APR-2004 (TREMBlrel. 27, Created)		
AC AAS52294; DT 23-APR-2004 (TREMBlrel. 27, Last sequence update)		
AC AAS52294; DT 23-APR-2004 (TREMBlrel. 27, Last annotation update)		
GN ADR374CP.		
GN Ashbya gossypii (Yeast) (Bremothecium gossypii).		
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;		
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.		
OX NCBI_TaxID=33169;		
RN [1]		
SEQUENCE FROM N.A.		
RC STRAIN=ATCC 10895;		
RX PubMed=15001715;		
RA Dietrich F.S.; Voegelei S.; Brachat S.; Lerch A.; Gates K.; Steiner S.,		
RA Mohr C.; Philippson P.; Choi P.; Luedi P.; Gaffney T.,		
RA Dierfaff F.S.; Voegelei S.; Brachat S.; Dietrich F.S.; Lerch A.; Gaffney T.,		
RA "The Ashbya gossypii genome as a tool for mapping the ancient		
RT Saccharomyces cerevisiae genome.",		
RT Science 304:304-307 (2004).		
RL [2]		
SEQUENCE FROM N.A.		
RC STRAIN=ATCC 10895;		
RA Voegelei S.E.; Brachat S.; Dietrich F.S.; Lerch A.; Gaffney T.,		
RA Philippson P.; Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.		
EMBL; AE016893; AAS52294.1; -.		
SEQUENCE 1640 AA; 182887 MW;		
Query Match 92.1%; Score 35; DB 2; Length 1640;		
Best Local Similarity 75.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;		
Matches 6; Conservative 0; MisMatches 0; Indels 0; Gaps 0;		
QY 1 FXXKYNFD 8		
Db 326 FSEKYNFD 333		
RESULT 14		
Q759A3 Q759A3 PRELIMINARY; PRT; 1640 AA.		
AC DT 05-JUL-2004 (TREMBlrel. 27, Created)		
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DE ADR374CP.		
Name-ADR374C.		
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).		
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;		
Saccharomycetales; Saccharomycetaceae; Bremothecium.		
NCBI TaxID=33169;		
[1]		
SEQUENCE FROM N.A.		
STRAIN=ATCC 10895;		
PubMed=15001715;		
Dierfaff F.S.; Voegelei S.; Brachat S.; Lerch A.; Gaffney T.,		
RA "The Ashbya gossypii genome as a tool for mapping the ancient		
RT Saccharomyces cerevisiae genome.",		
RT Science 304:304-307 (2004).		
RL [2]		
SEQUENCE FROM N.A.		
RC STRAIN=ATCC 10895;		
RA Voegelei S.E.; Brachat S.; Dietrich F.S.; Lerch A.; Gaffney T.,		
RA Philippson P.; Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.		
EMBL; AE016893; AAS52294.1; -.		
SEQUENCE 1640 AA; 182887 MW;		
Query Match 92.1%; Score 35; DB 2; Length 1640;		
Best Local Similarity 75.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;		
Matches 6; Conservative 0; MisMatches 0; Indels 0; Gaps 0;		
QY 1 FXXKYNFD 8		
Db 326 FSEKYNFD 333		

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OM protein - protein search, using sw model		Aar79132 Murine ki
Run on:	October 26, 2004, 15:19:44 ; Search time 44.6154 Seconds (without alignments) 64.324 Million cell updates/sec	Akr92708 Mouse p27 Aaw29718 27 kDa pr
Title:	US-09-574-735C-35	Aay08847 Murine wi
Perfect score:	40	Aay08819 Mouse wil
Sequence:	1 XIXGRYEW 8	Aab84650 Amnco ac1
Scoring table:	BLOSSM62	Aca62029 Mouse p27
Scoring table:	Gapext 10.0 , Gapext 0.5	Aay08841 Murine mu
Searched:	2000273 seqs, 358729299 residues	Aay08842 Murine mu
Total number of hits satisfying chosen parameters:	2002273	Aay08843 Murine mu
Minimum DB seq length:	0	Aay08844 Murine mu
Maximum DB seq length:	2000000000	Aay08845 Murine mu
Post-processing: Minimum Match %		Aay08846 Murine mu
Database :	A_Geneseq_23Seq04 : * 1: GeneseqP1900s: * 2: GeneseqP1900s: * 3: GeneseqP2000s: * 4: GeneseqP2001s: * 5: GeneseqP2002s: * 6: GeneseqP2003as: * 7: GeneseqP2003bs: * 8: GeneseqP2004s: *	RESULT 1 ID ABG65714 standard; peptide; 8 AA. XX ABG65714 ; XX AC XX DT 27-AUG-2002 (first entry) DB Plant ICK protein conserved motif 1 #22. DE Plant; inhibitor of cyclin dependent kinase; ICK. XX KW Plant; inhibitor of cyclin dependent kinase; ICK. XX OS Arabidopsis thaliana. XX PN WO200228893-A2. XX PR 14-JUL-2000; 20001WO-IB001492. XX PR 13-OCT-2000; 20000US-0218471P. XX PR 29-JUN-2001; 20000US-0241219P. XX PR 14-JUL-2000; 20001WO-IB001492. XX PD 11-APR-2002. XX PF XX XX (CROP-) CROPSDESIGN NV. XX PA XX PI Frankard VMS, Peres Bota AM, Drouai A, Mironov V, Inze D; XX PI Hatzfeld Y; XX DR WPI; 2002-471311/50. XX PS Disclosure: Page 14: 141PP; English.
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
Result No.	Score	Query Length DB ID Description
1	38	95.0 8 5 ABG65714 Plant ICK
2	38	95.0 53 5 ABG65677 Lobolly
3	38	95.0 136 3 AAY44339 Arabidops
4	38	95.0 137 5 AAB25107 Arabidops
5	38	95.0 216 2 AAW98180 Arabidops
6	38	95.0 222 5 AAB25111 Arabidops
7	38	95.0 222 8 ADN72351 Thale cre
8	37	92.5 8 5 ABG65721 Plant ICK
9	37	92.5 8 5 ABG65712 Plant ICK
10	37	92.5 22 5 ABG65671 OStICK 1 P
11	37	92.5 3 AAB26247 Soybean C
12	37	92.5 38 3 AAP01942 Soybean C
13	37	92.5 87 3 AAP01951 Cyclin de
14	37	92.5 87 3 AAB27533 Soybean C
15	37	92.5 138 2 AAY08846 Murine mu
16	37	92.5 138 2 AAY08818 Murine mu
17	37	92.5 171 3 AAG42859 Arabidops
18	37	92.5 171 3 AAG15427 Arabidops
19	37	92.5 183 2 AAY08845 Murine mu
20	37	92.5 183 2 AAY08840 Murine mu
21	37	92.5 183 2 AAY08812 Murine mu
22	37	92.5 183 2 AAY08817 Murine p27
23	37	92.5 191 3 AAY44335 Arabidops
24	37	92.5 191 3 AAG15426 Arabidops
25	37	92.5 191 3 AAG42858 Arabidops

OS Arabidopsis thaliana.
 XX WO200250292-A2.
 XX PR 18-DEC-2001; 2001WO-CA001825.
 XX PR 18-DEC-2000; 2000US-0255908P.
 (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 PA (U.S.A.-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 XX PA DNA encoding inhibitor of cyclin-dependent kinase.
 XX PI Wang H, Zhou Y, Powke LC;
 XX WPI; 2002-519888/55.
 DR N-PSDB; AAD40767.
 XX
 PT
 Disclosure; Fig 10A; 8pp; English.
 The invention relates to a method for the development of a plant. The method involves introducing into a plant cell a nucleic acid encoding a protein that binds or interacts with a cyclin-dependent kinase (CDK) inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN8 and ICDK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the degradation of a CDK inhibitor polypeptide. The method is useful for modifying the growth and development of plants e.g. morphogenesis, growth, multiplication, enlargement differentiation or maturation of a cell or plant. It is particularly useful in plant breeding. The present sequence is A. thaliana ICN7 partial protein
 XX SQ Sequence 137 AA;
 XX Query Match Score 38%; DB 5; Length 137;
 XX Best Local Similarity 85.7%; Pred. No. 11;
 XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX Qy 2 LXGRYEW 8
 XX Db 126 LSGRYEW 132
 XX
 RESULT 5
 ID AAW8180
 XX AAW8180 standard; protein; 216 AA.
 AC AAW8180;
 XX 05-JUL-1999 (first entry)
 DE Cyclin-dependent kinase inhibitor; CKI; CDKI; FL66.
 KW Plant development; transgenic plant; cell cycle; growth regulator;
 KW herbicide.
 XX OS Arabidopsis thaliana.
 XX Key Location/Qualifiers
 Protein 11..216
 /note= "this protein region is specifically claimed in
 Claim 1(c)"
 XX
 RESULT 6
 ID AAE25111
 XX AAE25111 standard; protein; 222 AA.
 AC AAE25111;
 XX DT 30-OCT-2002 (first entry)
 XX DE Arabidopsis thaliana ICN7 full-length protein.
 KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
 KW ICN2; ICN6; ICN7; ICN8; ICDK; morphogenesis; maturation; enlargement;
 KW plant breeding; growth.
 OS Arabidopsis thaliana.
 XX PN WO200250292-A2.
 XX PD 27-JUN-2002.
 XX PF 18-DEC-2001; 2001WO-CA001825.
 XX PR 18-DEC-2000; 2000US-0255908P.
 XX PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 PA (U.S.A.-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 PA Wang H, Zhou Y, Powke LC;
 XX DR 2002-519888/55.
 XX
 WO9914331-A2.
 XX Key Location/Qualifiers
 Protein 11..216
 /note= "this protein region is specifically claimed in
 Claim 1(c)"
 XX
 WO98NO-EP005895.
 XX
 WO98NO-EP005895.

DR N-PSDB; AAD40771.
 XX Modifying plant development, e.g. growth or maturation, which is
 PT particularly useful in plant breeding, by introducing nucleic acids
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
 PT that bind to CDK inhibitors.
 XX Disclosure; Fig 10B; 8pp; English.
 CC The invention relates to a method for the development of a plant. The
 CC method involves introducing into a plant cell a nucleic acid encoding a
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK),
 CC inhibitor polypeptide (such as ICK1, ICK2, ICK5, ICN7, ICN8 and
 CC ICN9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
 CC degradation of a CDK inhibitor polypeptide. The method is useful for
 CC modifying the growth and development of plants e.g. morphogenesis,
 CC growth, multiplication, enlargement, differentiation or maturation of a
 CC cell or plant. It is particularly useful in plant breeding. The present
 CC sequence is A. thaliana ICN7 full-length protein
 XX Sequence 222 AA;
 SQ Query Match 95.0%; Score 38; DB 5; Length 222;
 Best Local Similarity 85.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LXGRYEW 8
 Db 211 LSGRYEW 217

RESULT 7
 ADN72351 standard; protein; 222 AA.
 ID ADN72351
 XX AC ADN72351;
 XX DT 15-JUL-2004 (first entry)
 DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 246.
 XX plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
 KW animal feed product; thale cress; cell wall biosynthesis;
 KW nitrogen metabolism; carbon metabolism.
 XX Arabidopsis thaliana.
 OS WO2004035798-A2.
 PN 29-APR-2004.
 PR 20-OCT-2003; 2003WO-EP011658.
 PR 18-OCT-2002; 2002EP-00079408.
 XX (CROP-) CROPDFSIGN NV.
 PA Inze D, De Veylder L, Vlieghe K;
 XX WPI; 2004-348466/32.
 DR N-PSDB; ADN72350.
 XX Altering plant characteristics useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX Claim 1; SEQ ID NO 246; 134pp; English.
 PS This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to

CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture,
 CC or physiology, altered endoreduplication, biochemistry, signal
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polypeptide sequence is thale cress protein
 CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
 CC the E2Fa/Dpa transcription factor, given in an exemplification of the
 CC invention.
 XX Sequence 222 AA;
 SQ Query Match 95.0%; Score 38; DB 8; Length 222;
 Best Local Similarity 85.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LXGRYEW 8
 Db 211 LSGRYEW 217

RESULT 8
 ABG65721 standard; peptide; 8 AA.
 ID ABG65721
 XX AC ABC65721;
 XX DT 27-AUG-2002 (first entry)
 XX DE Plant ICK protein conserved motif 1 #29.
 XX KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX OS Oryza sativa.
 XX PN WO200228893-A2.
 XX PD 11-APR-2002.
 XX PF 29-JUN-2001; 2001WO-1B001492.
 XX PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX PA (CROP-) CROPDFSIGN NV.
 XX PI Frankard VMS, Peres Botta AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX DR; 2002-471311/50.
 XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.
 XX Disclosure; Page 14; 141pp; English.
 XX This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC insufficient or excessive production of an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally-occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to

CC ICK wild type protein. The present sequence represents an inhibitor of
CC cyclin dependent kinase (ICK) protein of the invention

SQ Sequence 8 AA;

Query Match	92.5%	Score 37;	DB 5;	Length 8;
Best Local Similarity	85.7%	Pred. No.	1.7e+06;	
Matches	6;	Mismatches	0;	Gaps 0;
Qy.	2 LXGRYEW 8			
Db	2 LQGRYEW 8			

SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Gaps 0;

Indels 0;

CC cyclin dependent kinase; ICK.

CC Arabidopsis thaliana.

CC WO200228893-A2.

XX PD 11-APR-2002.

XX AC ABG65712;

XX DT 27-AUG-2002 (first entry)

XX DE Plant ICK protein conserved motif 1 #20.

XX JN Plant; inhibitor of cyclin dependent kinase; ICK.

XX OS Arabidopsis thaliana.

XX PN WO200228893-A2.

XX XX PD 11-APR-2002.

XX XX PR 29-JUN-2001; 2001WO-IB001492.

XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used

PT to screen substrates, drugs or compounds which modulate ICK activity and

PT treat disorders characterized by an insufficient or excessive production

PT of ICK inhibitors.

XX PS Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

XX PI Hatzfeld Y;

XX DR 2002-471311/50.

XX XX WPI; 2002-471311/50.

XX XX N-PDB; ABK93951.

XX XX (CROP-) CROBDESIGN NV.

XX XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;

XX PI Hatzfeld Y;

XX DR 2002-471311/50.

XX XX WPI; 2002-471311/50.

XX XX PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used

PT to screen substrates, drugs or compounds which modulate ICK activity and

PT treat disorders characterized by an insufficient or excessive production

PT of ICK inhibitors.

XX PS Disclosure: Page 14; 141pp; English.

XX CC This invention relates to the DNA and protein sequences of novel isolated

CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of

CC the invention may be used for treating disorders characterised by

CC insufficient or excessive production of an ICK inhibitor. The protein of

CC the invention may also be used to screen for naturally-occurring ICK

CC substrates, drugs or compounds which modulate ICK activity, as well as to

CC treat disorders characterised by insufficient or excessive production of

CC ICK protein, forms which have decreased or aberrant activity compared to

CC ICK wild type protein. The present sequence represents an inhibitor of

CC cyclin dependent kinase (ICK) protein of the invention

SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 2.6;

Mismatches 0;

Conservative 0;

Indels 0;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

DB 5; Length 8;

Pred. No. 1.7e+06;

Mismatches 0;

Conservative 1;

Indels 1;

Gaps 0;

CC

CC Best Local Similarity 85.7%; Pred. No. 1.7e+06;

CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC SQ Sequence 8 AA;

Query Match

92.5%; Score 37;

OS Glycine max.
 XX WO200060087-A2.
 XX PN
 PD 12-OCT-2000.
 XX PP 06-APR-2000; 2000WO-US009106.
 XX PR 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Klein TM, Weng Z, Cahoon RE;
 PI DR; 2000-679375/66.
 DR N-PSDB, AAN02392.
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX PS Claim 10; Page 42; 58pp; English.

XX The present sequence is the soybean cyclin-dependent kinase inhibitor (CDKI). Its coding sequence was isolated by searching a soybean seedling cDNA library for sequences similar to those encoding the CDKI from Chenorodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides in genetic and physical mapping and in the isolation of the CDKI gene in other organisms.

XX Sequence 38 AA;
 SQ Query Match Score 37; DB 3; Length 38;
 Best Local Similarity Pred. No. 4.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX Qy 2 LXGRYEW 8
 Db 27 LEGRYEW 33

XX RESULT 13
 AAP01951 ID AAP01951 standard; protein; 87 AA.
 XX AC AAP01951;
 XX DT 01-NOV-2001 (first entry)
 XX DE Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0008.d2:fis.
 XX KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
 KW plant growth inhibitor.
 XX OS Glycine max.
 XX PN WO200060087-A2.
 XX PD 12-OCT-2000.
 XX PP 06-APR-2000; 2000WO-US009106.
 XX PR 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Klein TM, Weng Z, Cahoon RE;
 PI DR; 2000-679375/66.
 DR N-PSDB, AAN02401.
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.

XX PS Claim 10; Fig 1; 58pp; English.

XX The invention describes a novel isolated polynucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDKI or affects the level of CDKI expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDKI. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as Genetic markers. The sequence is the soybean CDKI clone s12.pk0008.d2 as described in the method of the invention

XX Sequence 38 AA;
 SQ Query Match Score 37; DB 3; Length 38;
 Best Local Similarity Pred. No. 4.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX Qy 2 LXGRYEW 8
 Db 27 LEGRYEW 33

XX RESULT 13
 AAP01951 ID AAP01951 standard; protein; 87 AA.
 XX AC AAP01951;
 XX DT 01-NOV-2001 (first entry)
 XX DE Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0008.d2:fis.
 XX KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
 KW plant growth inhibitor.
 XX OS Glycine max.
 XX PN WO200060087-A2.
 XX PD 12-OCT-2000.
 XX PP 06-APR-2000; 2000WO-US009106.
 XX PR 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Klein TM, Weng Z, Cahoon RE;
 PI DR; 2000-679375/66.
 DR N-PSDB, AAN02401.
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.

XX PS Claim 10; Fig 1; 58pp; English.

XX The invention describes a novel isolated polynucleotide comprising a nucleotide sequence encoding one of 17 specific cyclin dependent kinase inhibitor (CDKI) polypeptides, cell cycle regulators involved in control of cell division, growth and death. The nucleotide sequences can be used in a vector to transform a host cell to produce the CDKI polypeptide. They can also be used in methods for selecting and obtaining a nucleic acid sequence that encodes CDKI or affects the level of CDKI expression.

The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDK1. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the soybean CDK1 clone s12.pk008.d2:fs as described in the method of the invention

XX

SQ Sequence 87 AA;

Query Match 92.5%; Score 37; DB 3; Length 87;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
 Db 76 LEGRYEW 82

XX

RESULT 14

AAB27253

ID AAB27253 standard; protein; 87 AA.

XX

AC AAB27253;

XX

DT 17-JAN-2001 (first entry)

XX

DE Soybean cyclin-dependent kinase inhibitor #2.

XX

KW Scybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;

XX

KW CDK1; cell growth; herbicide.

XX

OS Glycine max.

XX

PN WO2000060087-A2.

XX

PD 12-OCT-2000.

XX

PP 06-APR-2000; 2000WO-US009106.

XX

PR 07-APR-1999; 99US-0128132P.

XX

PA (DUPONT) DU PONT DE NEMOURS & CO E I.

XX

PI Klein TM, Weng Z, Cahoor RE;

XX

WPI: 2000-679375/66.

DR N-PSDB; AA995287.

XX

PT Cyclin dependent kinase inhibitor sequences, useful for identifying

PT herbicides and plant growth inhibitors.

XX

PS Claim 10; Fig 1; 58pp; English.

XX

The present sequence is the soybean cyclin-dependent kinase inhibitor (CDK1). Its coding sequence was isolated by searching the soybean seedling cDNA library for sequences similar to those encoding the CDK1 from Chenopodium rubrum, *Cnephobaditis elegans* and *Arabidopsis thaliana*. CDK1 is involved in the cell cycle, and may promote or inhibit cell division and growth. The protein and its coding sequence are useful in the production of transgenic plants which produce increased or decreased amounts of the CDK1 protein, in the identification of herbicides, in genetic and physical mapping, and in the isolation of the CDK1 gene in other organisms

XX

SQ Sequence 87 AA;

XX

Query Match 92.5%; Score 37; DB 3; Length 87;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8

Db 76 LEGRYEW 82

RESULT 15

AAV08846

AAV08846 standard; protein; 138 AA.

XX

AC AAV08846;

XX

DT 13-AUG-1999 (first entry)

XX

XX Murine mutant p27 protein from clone #850.

XX DE

KW p163; murine p27 inhibitor; p27-induced inhibition; cell proliferation; tumour; mutant; p27 protein.

XX

OS Mus sp.

XX

EP26236-A1.

XX

PD 30-JUN-1999.

XX

PF 12-DEC-1998;

XX

PR 20-DEC-1997;

XX

PA (HMR) HOECHST MARION ROUSSEL DEUT GMBH.

XX

PI Eilers N, Buergin A, Sedlacek H;

XX

WPI: 1999-349237/30.

XX

PT New p27-inhibiting protein p163 and DNA - useful for detection and/or quantification of p163 mRNA.

XX

DR WPI: 1999-349237/30.

XX

PS Disclosure; Page 28; 68pp; German.

XX

PR XX

CC This invention describes (1) a protein that inhibits p27 and thereby arrests p27-induced inhibition of cell proliferation, (2) the protein of (1) comprising at least part of the amino acid sequence of murine p163.

CC (3) a protein that can be derived from the protein of (2) by deletion of (3) the p27 binding domain or the Ran binding domain, (4) a protein that can be derived from the protein of (2) by deletion of all amino acid sequences other than the p27 binding domain, (5) a protein that is the human or other mammalian species homologue of a protein as in (1)-(4), (6) DNA encoding the p163 protein, (7) antibodies and antibody fragments that bind to the p27 binding domain of a protein as above, (8) antibodies and antibody fragments that bind to the Ran binding domain of a protein as above, (9) antisense nucleic acids complementary to portions of the DNA between codons 121 and 467, (10) a nucleic acid construct coding for an antisense nucleic acid as in (9) for inhibiting the proliferation of a cell, in which DNA coding for the antisense nucleic acid sequence is linked to at least one activation sequence and is introduced into the target cell as naked DNA or as an insert in a viral vector and (11) a nucleic acid construct containing the DNA of (6) linked to an activation sequence that permits expression of a protein as above in a cell. The DNA of (6) can be used for detection and/or quantification of p163 mRNA in cells and/or tissues, preferably by Northern blotting, PCR or fluorescent in-situ hybridisation. The proteins can be used to produce antibodies, which can be used to detect the corresponding protein in cells, tissues or body fluids. The antisense nucleic acids can be used to inhibit cell proliferation in vitro or in vivo. The proteins can be used to screen for substances that inhibit the interaction between the proteins and their cellular binding partners, preferably using a two hybrid system or using an affinity system in which p163 or its p27-binding domain is immobilized on a solid phase, the solid phase is incubated with a test substance, and the inhibition of the binding of a labelled binding partner of p163 (especially p27 or Ran) is measured. Assays for p163 can be used to assess the malignancy of tumours. This sequence represents a mutant mouse p27 protein sequence isolated from Clone #86 which is used to describe the method of the invention

CC

XX

SQ Sequence 138 AA:
Query Match 92.5%; Score 37; DB 2; Length 138;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LXGRYEW 8
| |||||
Db 55 LBGRYEW 61

Search completed: October 26, 2004, 15:36:52
Job time : 45.6154 secs

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 I protein - protein search, using sw model
 run on: October 26, 2004, 15:19:44 ; Search time 13.2308 Seconds
 (without alignments)
 40.099 Million cell updates/sec
 title: US-09-574-735C-35
 rfect score: 40
 quence: 1 XLXGRYEW 8
 oring table: BL051N62
 Gapop 10.0 , Gapext 0.5
 Sequence 6, AppLi
 Sequence 6, AppLi
 Sequence 6, AppLi
 Sequence 1, AppLi
 Sequence 3, AppLi
 Sequence 4, AppLi
 Sequence 2, AppLi
 Sequence 6, AppLi
 Sequence 2, AppLi
 Sequence 22, AppLi
 Sequence 2, AppLi
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Minimum DB seq length: 0

Post-processing:

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red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. This is derived by analysis of the total score distribution.

SUMMARIES

כטבָּה

RESULT 1
US-09-526-597D-4
; Sequence 4, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veljder, Lieven
; APPLICANT: de Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinassase
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-09-526-597D-4

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RESULT 2
US-09-215-221-56
; Sequence ID: Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
;   APPLICANT: EILERS, MARTIN
;   APPLICANT: BURGIN, ANDREA
;   APPLICANT: SEDLACEK, HANS HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
;   INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026063/0192
; CURRENT APPLICATION NUMBER: US/09/215-221
; CURRENT FILING DATE: 1998-12-18
; PRIORITY NUMBER: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 56
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Myrmeleon sp
Query Match      95.1%; Score 38; DB 4; Length 222;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy          2 LXGREGIEW 8
Db          211 LSGRGEW 217

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FEATURE INFORMATION: mutated p27
US-09-215-221-56

Query Match 92.5%; Score 37; DB 3; Length 135;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 LXGRYEW 8
Db 55 LEGRYEW 61

RESULT 5
US-09-215-221-53
Sequence 53, Application US/09215221
Patent No. 6255562

GENERAL INFORMATION:
APPLICANT: BILERS, MARTIN
APPLICANT: BUERGIN, ANDREA
APPLICANT: SEDLACEK, HANS-HARALD
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
FILE REFERENCE: 026083/0192
CURRENT APPLICATION NUMBER: US/09/215, 221
CURRENT FILING DATE: 1998-12-18
PRIORITY NUMBER: 1997-12-20
PRIORITY FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 50
LENGTH: 180
TYPE: PRT
ORGANISM: Murine sp.
OTHER INFORMATION: mutated p27
US-09-215-221-53

Query Match 92.5%; Score 37; DB 3; Length 193;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 LXGRYEW 8
Db 65 LEGRYEW 71

RESULT 6
US-09-215-221-51
Sequence 51, Application US/09215221
Patent No. 6255562

GENERAL INFORMATION:
APPLICANT: BILERS, MARTIN
APPLICANT: BUERGIN, ANDREA
APPLICANT: SEDLACEK, HANS-HARALD
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
FILE REFERENCE: 026083/0192
CURRENT APPLICATION NUMBER: US/09/215, 221
CURRENT FILING DATE: 1998-12-18
PRIORITY NUMBER: 1997-12-20
PRIORITY FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 51
LENGTH: 194
TYPE: PRT
ORGANISM: Murine sp.
FEATURE:
OTHER INFORMATION: mutated p27
US-09-215-221-51

Query Match 92.5%; Score 37; DB 3; Length 194;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 LXGRYEW 8
Db 65 LEGRYEW 71

Query Match 92.5%; Score 37; DB 3; Length 180;
Best Local Similarity 85.7%; Pred. No. 5.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 2 LXGRYEW 8
Db 55 LEGRYEW 61

RESULT 4
US-09-215-221-55
Sequence 55, Application US/09215221
Patent No. 6255562

GENERAL INFORMATION:
APPLICANT: BILERS, MARTIN
APPLICANT: BUERGIN, ANDREA
APPLICANT: SEDLACEK, HANS-HARALD
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
FILE REFERENCE: 026083/0192
CURRENT APPLICATION NUMBER: US/09/215, 221
CURRENT FILING DATE: 1998-12-18
PRIORITY NUMBER: 1997-12-20
PRIORITY FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 180
TYPE: PRT
ORGANISM: Murine sp.
FEATURE:
OTHER INFORMATION: mutated p27
US-09-215-221-55

Query Match 92.5%; Score 37; DB 3; Length 180;

Db 66 LEGRYEW 72

RESULT 7
US-09-215-221-52; Sequence 52, Application US/09215221
; Patent No. 6265562

; GENERAL INFORMATION:

; APPLICANT: EILRS, MARTIN

; APPLICANT: BURGIN, ANDREA

; APPLICANT: SEDLACEK, HANS-HARALD

; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY

; FEATURES: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/215 221

; PRIOR APPLICATION NUMBER: 1998-12-18

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 52

; LENGTH: 194

; TYPE: PRT

; ORGANISM: Murine sp.

; FEATURE:

; OTHER INFORMATION: mutated p27

US-09-215-221-52

Query Match
Best Local Similarity 92.5%; Score 37; DB 3; Length 194;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8

Db 66 LEGRYEW 72

RESULT 8

US-09-215-221-54

; Sequence 54, Application US/09215221
; Patent No. 6265562

; GENERAL INFORMATION:

; APPLICANT: EILRS, MARTIN

; APPLICANT: BURGIN, ANDREA

; APPLICANT: SEDLACEK, HANS-HARALD

; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY

; FEATURES: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF

; FILE REFERENCE: 026083/0192

; CURRENT APPLICATION NUMBER: US/09/215, 221

; PRIOR APPLICATION NUMBER: 1998-12-18

; PRIOR FILING DATE: 1997-12-20

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO: 54

; LENGTH: 195

; TYPE: PRT

; ORGANISM: Murine sp.

; FEATURE:

; OTHER INFORMATION: mutated p27

US-09-215-221-54

Query Match
Best Local Similarity 92.5%; Score 37; DB 3; Length 195;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8

Db 67 LEGRYEW 73

RESULT 9

US-09-275-983B-2

; Sequence 2, Application US/08275983B
; Patent No. 5688665
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Robert, James M.
; APPLICANT: Roff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid Molecules
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READEABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275, 983B
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179, 045
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36, 709
; TELECOMMUNICATION INFORMATION: MIT-079CP
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-275-983B-2

Query Match
Best Local Similarity 92.5%; Score 37; DB 1; Length 197;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76

RESULT 10

US-08-415-655-6

; Sequence 6, Application US/08415655
; Patent No. 6025580
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Lee, Mong-hong
; TITLE OF INVENTION: ISOLATED NUCLEAR ACID MOLECULES ENCODING
; TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: United States of America
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READEABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 1747/4741B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-415-655-6

Query Match 92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5%;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76

RESULT 11
US-09-240-906-B
Sequence 8, Application US/09240906
Patent No. 6245965
GENERAL INFORMATION:
APPLICANT: BOUSSEL, MARTINE F.
APPLICANT: SMEYNE, RICHARD
APPLICANT: ZINDY, FREDERIQUE
APPLICANT: CUNNINGHAM, JUSTINE
TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: 1340-0-1-025
CURRENT APPLICATION NUMBER: US/09/240,906
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NCS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
TYPE: PRT
ORGANISM: Mus musculus
US-09-240-906-B

Query Match 92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5%;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76

RESULT 12
US-09-215-221-57
Sequence 57, Application US/09215221
Patent No. 6265562
GENERAL INFORMATION:
APPLICANT: ELLERS, MARTIN
APPLICANT: BURGIN, ANDREA
APPLICANT: SEDLACK, HANS-HARALD

TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY CYCLIN-DEPENDANT KINASES AND USES THEREOF
TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
FILE REFERENCE: 026053 /0122
CURRENT APPLICATION NUMBER: US/09/215,221
CURRENT FILING DATE: 1998-12-18
PRIORITY APPLICATION NUMBER: 1997-56 975.7
PRIOR FILING DATE: 1997-12-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 197
TYPE: PRT
ORGANISM: Murine sp.
US-09-215-221-57

Query Match 92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5%;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76

RESULT 13
US-08-794-002-4
Sequence 4, Application US/08794002
Patent No. 6316208
GENERAL INFORMATION:
APPLICANT: Roberts, James M.
APPLICANT: Porter, Peggy L.
TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS PRODUCTION AND USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/794,002
APPLICATION NUMBER: US/08/794,002
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE DOCKET NUMBER: MTV-079.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-794-002-4

Query Match 92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5%;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76

RESULT 14
US-08-854-039B-4
; Sequence 4, Application US/08854039B
; Patent No. 6335774
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polak, Kornelia
; TITLE OF INVENTION: ISOLATED D27 PROTEIN AND METHOD FOR ITS
; NUMBER OF SEQUENCES: 27
; NUMBER OF INVENTION: PRODUCTION AND USE
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039B
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIY-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-854-039B-4
Query Match 92.5%; Score 37; DB 3; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76

RESULT 15
US-09-483-597-B
; Sequence 8, Application US/09483597
; Patent No. 6589505
; GENERAL INFORMATION:
; APPLICANT: ROUSSEL, MARTINE F.
; APPLICANT: SHEYNE, RICHARD
; APPLICANT: ZINDY, FREDERIQUE
; APPLICANT: CUNNINGHAM, JUSTINE
; APPLICANT: SEJIL, NEIL
; APPLICANT: CHEN, FING
; TITLE OF INVENTION: CELLS THAT LACK P19INK4D AND P27KIP1 ACTIVITY AND
; METHODS OF USE THEREOF
; FILE REFERENCE: 13-0-1-025N
; CURRENT APPLICATION NUMBER: US/09/483,597
; CURRENT FILING DATE: 2000-01-14
; EARLIER APPLICATION NUMBER: 60/117,719
; EARLIER FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

; LENGTH: 197
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-483-597-B
Query Match 92.5%; Score 37; DB 4; Length 197;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76
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Job time : 13.2308 secs



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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 115.077 Seconds
(without alignments)
22.507 Million cell updates/sec

Title: US-09-574-735C-35
Perfect score: 40
Sequence: 1.XIXGYEW 8

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	38	95.0	53	15 US-10-333-006-17 Sequence 17, Appl
2	38	95.0	132	16 US-10-437-933-199574 Sequence 5128, A
3	38	95.0	137	9 US-09-733-507-14 Sequence 14, Appl
4	38	95.0	137	15 US-10-451-139-13 Sequence 13, Appl
5	38	95.0	222	15 US-10-68-291-4 Sequence 4, Appl
6	38	95.0	222	15 US-10-451-139-21 Sequence 21, Appl
7	38	95.0	224	15 US-10-424-999-210190 Sequence 210190,
8	37	92.5	22	15 US-10-333-006-11 Sequence 11, Appl
9	37	92.5	48	15 US-10-424-519-153517 Sequence 15317,
10	37	92.5	191	9 US-09-733-507-2 Sequence 2, Appl
11	37	92.5	191	9 US-09-733-507-10 Sequence 10, Appl
12	37	92.5	191	15 US-10-451-139-2 Sequence 2, Appl
13	37	92.5	197	9 US-09-865-018-4 Sequence 4, Appl

Sequence 182928,
Sequence 198574,
Sequence 43638, A
Sequence 1161, Appl
Sequence 36263, A
Sequence 235800,
Sequence 128205,
Sequence 6, Appl
Sequence 77900, A
Sequence 59718, A
Sequence 61054, A
Sequence 37255, A
Sequence 12275, A
Sequence 20, Appl
Sequence 18, Appl
Sequence 11, Appl
Sequence 212181,
Sequence 10, Appl
Sequence 6, Appl
Sequence 12, Appl
Sequence 16, Appl
Sequence 15, Appl
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Sequence 1164, Appl
Sequence 303, App
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Sequence 2, Appl
Sequence 19, Appl

ALIGNMENTS

RESULT 1
 Sequence 17, Application US/10333006
 / Publication No. US20040019926A1
 / GENERAL INFORMATION:
 / APPLICANT: Frankard, Valerie Marie-No. US20040019926A1le S.
 / APPLICANT: Perez Bota, Adrian Marius
 / APPLICANT: Droual, Anne-Marie
 / APPLICANT: Mironov, Vladimir
 / APPLICANT: Inz, Dirk
 / APPLICANT: Hatzfeld, Yves
 / TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
 / CURRENT APPLICATION NUMBER: US/10/333,006
 / CURRENT FILING DATE: 2003-01-14
 / PRIORITY APPLICATION NUMBER: PCT/IB01/01492
 / PRIORITY FILING DATE: 2001-06-29
 / PRIORITY APPLICATION NUMBER: US 60/218,471
 / PRIORITY FILING DATE: 2000-07-14
 / PRIORITY FILING DATE: US 60/241,219
 / PRIORITY FILING DATE: 2000-10-13
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 17
 / LENGTH: 53
 / TYPE: PRT
 / ORGANISM: Pinus taeda
 US-10-333-006-17
 Query Match 95.0% ; Score 38; DB 15; Length 53;
 Best Local Similarity 95.7%; PrdNo. 7.6;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGYEW 8
 Db 42 LSGRYEW 48

PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 21
; LENGTH: 222
; TYPE: PRT
; ORGANISM: *Arabidopsis thaliana*
US-10-451-139-21

Query Match 95.0%; Score 38; DB 15; Length 22;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 211 LSGRYEW 217

RESULT 7
US-10-424-599-210190
; Sequence 210190, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 210190
; LENGTH: 224
; TYPE: PRT
; FEATURE: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_10964C.1.dep

Query Match 95.0%; Score 38; DB 15; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 213 LSGRYEW 219

RESULT 8
US-10-333-006-11
; Sequence 11, Application US/10333006
; Publication No. US2004001992A1
; GENERAL INFORMATION:
; APPLICANT: Frankard, Valerie Marie-NO US20040019926A11e S.
; APPLICANT: Peres Bota, Adrian Marius
; APPLICANT: Droual, Anne-Marie
; APPLICANT: Mironov, Vladimir
; APPLICANT: Inz, Dirk
; APPLICANT: Hatzfeld, Yves
; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
; FILE REFERENCE: 118-13
; CURRENT APPLICATION NUMBER: US/10/333,006
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: PCT/IB01/01492
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/218,471
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/241,219
; PRIOR FILING DATE: 2000-10-13

Query Match 92.5%; Score 37; DB 9; Length 191;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 9
US-10-424-599-153517
; Sequence 153517, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 153517
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_10964C.1.dep

Query Match 92.5%; Score 37; DB 15; Length 48;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 37 LGRYEW 43

RESULT 10
US-09-733-507-2
; Sequence 2, Application US/09733507
; Patent No. US010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: *Arabidopsis thaliana*

Query Match 92.5%; Score 37; DB 9; Length 191;

Qy 2 LXGRYEW 8 US-09-865-018-4
 Db 181 LEGRYEW 187 Sequence 4, Application US/09865018
 / Patent No. US200101088A1
 / GENERAL INFORMATION:
 / APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
 / TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
 / FILE REFERENCE: 81601-3
 / CURRENT APPLICATION NUMBER: US/09/733,507
 / PRIOR APPLICATION NUMBER: CA 2,256,121
 / PRIOR FILING DATE: 1998-12-31
 / NUMBER OF SEQ ID NOS: 16
 / SOFTWARE: Patentin Ver. 2.0
 / LENGTH: 191
 / SEQ ID NO: 10
 / TYPE: PRT
 / ORGANISM: Arabidopsis thaliana

US-09-733-507-10 Query Match 92.5%; Score 37; DB 9; Length 191;
 Best Local Similarity 85.7%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
 Db 181 LEGRYEW 187

RESULT 12 US-10-451-139-2 Query Match 92.5%; Score 37; DB 9; Length 197;
 Subsequence 2, Application US/10451139
 / Publication No. US20040098763A1
 / GENERAL INFORMATION:
 / APPLICANT: WANG, HONG
 / APPLICANT: ZHOU, YONGMING
 / APPLICANT: FOWKE, LARRY C.
 / APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF AGRICULTURE AND AGRI-FOOD CANADA
 / TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
 / TITLE OF INVENTION: ACTIVITY
 / FILE REFERENCE: 4810-62237
 / CURRENT APPLICATION NUMBER: US/10/451,139
 / CURRENT FILING DATE: 2003-06-18
 / PRIOR APPLICATION NUMBER: WO/PCT/CA01/01825
 / PRIOR FILING DATE: 2001-12-18
 / NUMBER OF SEQ ID NOS: 23
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO: 2 LENGTH: 191
 / TYPE: PRT
 / ORGANISM: Arabidopsis thaliana

US-10-451-139-2 Query Match 92.5%; Score 37; DB 15; Length 191;
 Best Local Similarity 85.7%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
 Db 181 LEGRYEW 187

RESULT 14 US-10-424-599-182928 Query Match 92.5%; Score 37; DB 9; Length 197;
 Subsequence 182928, Application US/10424599
 / Publication No. US20040031072A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J
 / APPLICANT: Kovacic, David J
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53223)B
 / CURRENT APPLICATION NUMBER: US/10/424,599
 / CURRENT FILING DATE: 2003-04-28
 / NUMBER OF SEQ ID NOS: 285684
 / SEQ ID NO: 18928 LENGTH: 205
 / TYPE: PRT
 / ORGANISM: Glycine max

Qy 2 LXGRYEW 8
 Db 181 LEGRYEW 187

RESULT 13

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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MET3847_13619BC.1.pep
US-10-424-599-182928

Query Match      92.5%; Score 37; DB 15; Length 205;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy          2 LXGRYEW 8
Db          194 LEGRYEW 200

RESULT 15
US-10-437-963-198574
Sequence 198574, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbozuk, Brad
; APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 198574
LENGTH: 225
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRF24530_9421C.1.pep
US-10-437-963-198574

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Query Match      92.5%; Score 37; DB 16; Length 225;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy          2 LXGRYEW 8
Db          203 LGRYEW 209

Search completed: October 26, 2004, 15:33:29
Job time : 115.077 secs

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30	31	77.5	73	2	A97975
	31	77.5	113	1	S40138
	32	77.5	131	1	RWHUAA
	33	77.5	144	2	HB1823
	34	77.5	146	2	F11263
	35	77.5	164	2	C81629
	36	77.5	178	2	H80026
	37	77.5	178	2	F91180
	38	77.5	195	2	A82657
	39	77.5	217	1	H71208
	40	77.5	236	2	G82378
	41	77.5	242	2	S47756
	42	77.5	260	2	HB4060
	43	77.5	355	2	C70194
	44	77.5	420	2	E70914
	45	77.5	472	2	S37955

searched: 283416 seqs, 96216763 residues

total number of hits satisfying chosen parameters: 263410
minimum DB seq length: 0
RESULT 1
T01132 - *Neurobionics rhaliana* [Neurobionics]

cyclin-dependent kinase inhibitor protein [Langzeit] - AIAUWPFPS-ESIARQ
 N;Alternate names: hypothetical protein F26Bp_8
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999
 C;Accession: T01132; F84424
 Minimum Match 0%
 Maximum Match 100%
 Minimum Match 45%
 Maximum Match 45%
 Minimum Match 45%
 Maximum Match 45%

LIBRARY LIST *3 summarized
PIR 79:
1: PIR:
database :
A/Description: Arabidopsis thaliana chromosome II BAC F22B6 genomic sequence.
R/Rounseley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crobby, M.L.; Brandon, R.C.
Submitted to the EMBL Data Library June 1998

2: pir2:*

3: pir3:*

4: pir4:*

A,Reference number: Z14198

A,Accession: T01132

A,Status: translated from GB/EMBL/DDBJ

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, A; Molecule type: DNA
A; Residues: 1-191 <ROU>
A; Cross-references: UNIPROT:OB2809; EMBL:AC003040; NID:93242700; PID:93242706
A; Cross-references: cultivar:Colombia

	Score	Query Length	DB Length	TD	Description
result	%	match	match	match	Nierman et al., 1999

2 37 92.5 197 2 C83904
2 37 92.5 234 2 C83958
3 36 90.0 231 2 AI0271
4 36 90.0 231 2

A: Cross references: GB:AE002093; NLD:93242706; PTDN: AAC23.26.1; GSE:DB:GN0133
 C: Genetics:
 A: Gene: F26B6.8; At2g22430

				A;Map position:
				2
8	34	85.0	195	H96512
9	34	85.0	196	T09958

A;introns: 66/3; 81/2; 170/2

	Query	Match	Score	DB 2;	Length	191;
	Best Local Similarity			Prod. No.	3-6;	
10	34	85.0	198	2	T46140	
11	34	85.0	209	2	G83487	
12	34	85.0	314	2		

					RESULT 2
18	3.4	85.0	888	2	SIBSvS
19	3.4	85.0	888	2	SIBSvS
20	3.3	62.5	258	2	T23957

I49064 cyclin-cdk inhibitor p27 - mouse
N-Acetyl names: CDI B27; G1 cyclin-cyclin-dependent kinase inhibitor p27

```

C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C:Accession: TAanc6

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R.Toyoshima, H.; Hunter, T.
Cell 78, 67-74, 1994.

A;Reference number: A54839; MUID:94306519; PMID:8033213
A;Accession: I49064
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-197 <RES>
A;Cross-references: UNIPROT:P46414; EMBL:U10440; NID:9532771; PIDN:AAA21149_1; PID:9532771
C;Keywords: cell cycle control

Query Match Score 37; DB 2; Length 197;
Best Local Similarity 85.7%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 70 LEGRYEW 76

RESULT 3
C83587
hypothetical protein PA0162 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C;Species: *Pseudomonas aeruginosa*
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83587
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Bickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.I.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A829350; MUID:20437337; PMID:10984043
A;Accession: C83587
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-334 <STO>
A;Cross-references: UNIPROT:Q91656; GB:AE004091; NID:99946320; PIDN:AAG0385
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0462

Query Match Score 37; DB 2; Length 234;
Best Local Similarity 85.7%; Pred. No. 4.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 87 LYGRYEW 93

RESULT 4
AI0271
L-ribulose-phosphate 4-epimerase (EC 5.1.3.4) [imported] - *Yersinia pestis* (strain C092)
C;Species: *Yersinia pestis*
C;Accession: AI0271
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.; Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11566360
A;Accession: AI0271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1231 <KRD>
A;Cross-references: UNIPROT:Q8ZEB3; GB:AL550842; PIDN:CAc91037_1; PID:915980231; GSPDB:C
C;Genetics:
A;Gen: arAD
C;Superfamily: L-ribulose-phosphate 4-epimerase
C;Keywords: Isomerase

Query Match Score 36; DB 2; Length 231;
Best Local Similarity 71.4%; Pred. No. 7;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 334 VTGRYEW 340

RESULT 5
A75022
hypothetical protein PAB1224 - *Pyrococcus abyssi* (strain Orsay)
C;Species: *Pyrococcus abyssi*
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75022
R;Anonymous, Genoscope submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Accession number: A75001
A;Accession: A75022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <RAW>
A;Cross-references: UNIPROT:Q0UXZ7; GB:AJ248288; GB:AL096836; NID:95458960; PIDN:CAB5061
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1224
C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase
Query Match Score 35; DB 2; Length 216;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 53 MRGRYEW 59

RESULT 6
T36265
probable uroporphyrin-III C-methyltransferase / uroporphyrin-III synthase - *Streptomyces* sp.
C;Species: *Streptomyces coelicolor*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36265
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.; submitted to the EMBL Data Library, June 1999
A;Reference number: Z21576
A;Accession: T36265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-565 <MUR>
A;Cross-references: UNIPROT:Q9WX17; EMBL:AL079345; PIDN:CARB45351_1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3 (2)
C;Genetics:
A;Gene: SCOEDB_SCE68_15C
C;Superfamily: bifunctional uroporphyrin-III C-methyltransferase/uroporphyrinogen-III synthase
Query Match Score 35; DB 2; Length 565;
Best Local Similarity 71.4%; Pred. No. 28;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
Db 334 VTGRYEW 340

RESULT 7
T36005
hypothetical protein SCC22_15C - *Streptomyces coelicolor*
C;Species: *Streptomyces coelicolor*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36005
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.; submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
A;Accession: T36005
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
 A;Residues 1-144 <SEE>
 A;Cross-references: UNIPROT:Q9XAC3 ; EMBL:AL096839 ; PIDN:CAB50758_1 ; GSPPDB:GN00070 ; SCOED
 C;Genetics:
 A;Gene: SCODEB:SCC22_15C
 C;Superfamily: Streptomyces coelicolor hypothetical protein SCC22_15C

Query Match 85.0%; Score 34; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GRYEW 8
 Db 126 GRYEW 130

RESULT 8
 H96532
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: H96532
 P;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, B.; Hughes, B.; Huijzer, L.
 Nature 408: 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Lurois, J.S.; Maiti, R.; Mariotti, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tailion, S.L.; Schwartz, J.R.; Venter, J.C.; Davis, R.W.; Wu, D.; Yu, G.; Praser, C.M.; Venet, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; PMID:21016719; MUID:11130712
 A;Accession: H96532
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues 1-195 <STO>
 A;Cross-references: UNIPROT:Q9FX90 ; GB:AE005173 ; PIDN:G10120423 ; GSPPDB:G
 C;Genetics:
 A;Map position: 1

Query Match 85.0%; Score 34; DB 2; Length 195;
 Best Local Similarity 71.4%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
 Db 184 LEGRYEW 190

RESULT 9
 T09968
 C;Species: Chenopodium rubrum (red goosefoot)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T09968
 R;Fountain, M.D.; Renz, A.; Beck, E.
 A;Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic
 A;Reference number: Z16910
 A;Accession: T09968
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-196 <FOU>
 A;Cross-references: UNIPROT:Q4B537 ; EMBL:AJ002173
 A;Experimental source: photoautotrophic cells derived from hypocotyl tissue
 C;Genetics:
 A;Gene: CDK11
 C;Keywords: protein kinase inhibitor

Query Match 85.0%; Score 34; DB 2; Length 196;

Best Local Similarity 71.4%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
 Db 185 LKGRYDW 191

RESULT 10
 I52718
 Gene p2'kip1 protein - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C;Accession: I52718
 R;Rietepol, J.A.; Bohlander, S.K.; Sato, Y.; Papadopoulos, N.; Liu, B.; Friedman, C.; Cancer Res. 55, 1206-1210, 1995
 A;Title: Assignment of the human p2'kip1 gene to 12p13 and its analysis in leukemias.
 A;Reference number: I52718
 A;Accession: I52718
 A;Cross-references: UNIPROT:Q96TBO ; GB:S76988 ; NID:9998402 ; PIDN:AA014244_1 ; PID:942619
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-198 <RES>
 A;Cross-references: UNIPROT:Q96TBO ; GB:S76988 ; NID:9998402 ; PIDN:AA014244_1 ; PID:942619
 C;Genetics:
 A;Gene: p27kip1
 A;Introns: 159/1

Query Match 85.0%; Score 34; DB 2; Length 198;
 Best Local Similarity 71.4%; Pred. No. 15;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXGRYEW 8
 Db 70 LEGRYEW 76

RESULT 11
 T46140
 hypothetical protein T3A5.10 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: T46140
 R;Bloecker, H.; Meves, H.W.; Mayer, K.F.X.; Lemke, K.; Schueler, C.; Quetier, F.; Sal
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: Z223024
 A;Accession: T46140
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-209 <BL0>
 A;Cross-references: UNIPROT:Q9SCR2 ; EMBL:AU132979
 A;Experimental source: cultivar Columbia; BAC clone T3A5
 C;Genetics:
 A;Map position: 3
 A;Introns: 109/3 ; 130/2 ; 186/2
 A;Note: T3A5.10

Query Match 85.0%; Score 34; DB 2; Length 209;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GRYEW 8
 Db 200 GRYEW 204

RESULT 12
 G83487
 hypothetical protein PA1268 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Accession: G83487
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Folger, K.R.; Coulter, S.N.; Brody, K.; Larbig, K.; Kas,

A;Accession: A25196
 A;Molecule type: DNA
 A;Cross-references: 1-508 ; RP' ; 611-747 <COU>
 A;Cross-references: GB:D6562; NID:9473770; PIDN:BAA05598_1; PID:9473809
 A;Experimental source: strain K-12
 R;Fujita, N.
 submitted to the EMBL Data Library, January 1994
 A;Reference number: S45181
 A;Accession: S45219
 A;Molecule type: DNA
 A;Cross-references: EMBL:D26562; NID:9473770; PIDN:BAA05598_1; PID:9473809
 A;Experimental source: strain K-12, substrate W3110
 R;Burkhardt, R.; Brun, V.
 Mol. Gen. Genet. 209, 49-55, 1987
 A;Title: Nucleotide sequence of the fhuC and fhuD genes involved in iron (III) hydroxamate
 A;Reference number: A32650; MUID:2823072
 A;Accession: S06358
 A;Molecule type: DNA
 A;Residues: 723-747 <BUR>
 A;Cross-references: EMBL:X05810
 C;Genetics:
 A;Gene: fhuA; tonA
 A;Map position: 4 min
 C;Function:
 A;Description: located in the outer membrane, binds the ferrichrome-iron ligand; interact
 System
 C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
 C;Keywords: iron transport; membrane protein
 F1-33/Domain: signal sequence #status predicted <SIG>
 F134-747/Product: ferrichrome-iron receptor #status predicted <MAT>
 F198-235/Domain: tonB-dependent receptor amino-terminal homology <TN>
 F468-747/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
 Query Match Score 85.0%; Score 34; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 GRYEW 8
 Db 271 GRYEW 275
 RESULT 13
 S63401
 A;Hypothetical protein YNR069c - yeast (Saccharomyces cerevisiae)
 A;Alternative names: hypothetical protein N3555
 C;Species: Saccharomyces cerevisiae
 C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 03-Jul-2004
 C;Accession: S63401
 R;Duesterhoeft, A.; Fleeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 A;Submitted to the Protein Sequence Database, April 1996
 A;Reference number: S62944
 A;Accession: S63401
 A;Molecule type: DNA
 A;Residues: 1-489 <DUE>
 A;Cross-references: UNIPROT:P53755; EMBL:271684; NID:gi1302601; PID:e233850; PID:gi1302602
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: MIPS:YNR069c
 A;Cross-references: SGD:S00005352
 A;Map position: 14R
 Query Match Score 85.0%; Score 34; DB 2; Length 489;
 Best Local Similarity 71.4%; Pred. No. 38;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LXGRYEW 8
 Db 467 LRGYEW 473
 RESULT 14
 QRCFE
 A;Ferrichrome-iron receptor precursor - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 30-Jun-1988 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
 C;Accession: F47396; S4519; S06558
 A;Bacterium: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cole, R.; Rose, D.J.; Mau, B.; Shao, Y.
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: F64738
 A;Accession: F64720; MUID:9746617; PMID:9278503
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-747 <BLA>
 A;Cross-references: UNIPROT:P06971; GB:AE000124; GB:U00096; NID:gi1786339; PIDN: AAC73261.
 A;Experimental source: strain K-12, substrate MG1555
 R;Coulton, J.W.; Mason, P.; Cameron, D.R.; Carmel, G.; Jean, R.; Rode, H.N.
 J. Bacteriol. 165, 181-192, 1986
 A;Title: Protein fusions of beta-galactosidase to the ferrichrome-iron receptor of Esche
 A;Reference number: A35190; MUID:983362; PMID:200571
 Qy 2 LXGRYEW 8
 Db 462 LGGYDW 488



Copyright (C) 1993 - 2004	GenCore version 5.1.6	AAS89651	Yersinia
		Q9uxz7	pyrococcus
		Q6d5t0	erwinia car
		Q9wx17	streptomyce
		Q82e75	streptomyce
		Q96af4	homo sapien
		Q8xy31	ralsdonia s
		Q708j1	homo sapien
		Cae82383	homo sapien
		Q9xac3	streptomyce
		Q93yf6	nicotiana s
		Q43806	homo sapien
		Q9beas5	sus scrofa
		P46529	mustela vis
			ALIGNMENTS
Scoring table:	BLOSUM62		
Score:	Gapop 10.0 , Gapext 0.5		
Sequence:	US-09-574-735C-35		
Perfect score:	40		
Title:	XLIGREW 8		
Searched:	1825181 seqs, 575374646 residues		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing First 45 summaries		
Database :	Uniprot_02,*		
	1: uniprot_sprot:*		
	2: uniprot_trembl:*		
			Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
			SUMMARIES
Result No.	Score	Query Length	Description
1	38	95.0	Q8gt28 lycopersico
2	38	95.0	Q9fkbs5 arabidopsis
3	37	92.5	Q93v92 nicotiana t
4	37	92.5	Q6t220 glycine max
5	37	92.5	AAS11377 glycine m
6	37	92.5	Q6t221 glycine max
7	37	92.5	Aas13376 glycine m
8	37	92.5	Q04154 arabidopsis
9	37	92.5	Q82809 arabidopsis
10	37	92.5	Q8ldx1 arabidopsis
11	37	92.5	Q9fs28 pisum sativ
12	37	92.5	P46414 mus musculus
13	37	92.5	Q08769 rattus norvegicus
14	37	92.5	Q35792 ratmus norvegicus
15	37	92.5	Q8Bgt4 mung bean
16	37	92.5	Q6T2Z2 Glycine max
17	37	92.5	Q6Qmc3 anas platyrhynchos
18	37	92.5	Q8JIV2 gallus gallus
19	37	92.5	Aas02019 anas platyrhynchos
20	37	92.5	Aas13375 glycine max
21	37	92.5	Q6T2Z3 glycine max
22	37	92.5	Aas13374 glycine max
23	37	92.5	Q11656 pseudomonas
24	37	92.5	Qdjr3 synochococcus
25	36	92.0	Q9LR70 arabidopsis
26	36	90.0	Q9gt29 lycorensis
27	36	90.0	Q8ZEE3 yersinia pe
28	36	90.0	Q8D0U2 yersinia pe
29	36	90.0	Aas62245 yersinia
30	36	90.0	Q9cn07 pasteurella
31	35	87.5	Q6Pvn56 yersinia ru
			RESULT 1
			Q8G128
			PRELIMINARY;
			PRT; 185 AA.
		ID Q8G128;	
		AC Q8G128;	
		DT 01-MAR-2003 (TREMBLrel. 23, Created)	
		DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
		DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
		DB P27KIP1-related-protein 2.	
		GN Name=krp2;	
		OS Lycopersicon esculentum (Tomato).	
		OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;	
		OC Lamiales; Solanales; Solanaceae; Solanum.	
		NCBI_TaxID=4081;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RC TISSUE=Locular;	
		RA Bisebis B., Joubes J., Hernould M., Inze D., Raymond P., Chevalier C.,	
		RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.	
		DR EMBL; AU441250; CAD29619.1; -	
		DR GO:0005634; C-nucleus; IEA.	
		DR GO:0004861; Cyclin-dependent protein kinase inhibitor a...; IEA.	
		DR GO:0007050; Peiell cycle arrest; IEA.	
		DR InterPro:IPR003175; CDI.	
		DR PF02234; CDI; 1.	
		DR SQ SEQUENCE 185 AA; 21.89 MW; 48DCC89A5336C676 CRC64;	
		Query Match 95.0%; Score 38; DB 2; Length 185;	
		Best Local Similarity 85.7%; Pred. No. 12;	
		Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
		Qy 2 LXGRYEW 8	
		Db 174 LXGRYEW 180	
			RESULT 2
			Q9FKBS
			PRELIMINARY;
		ID Q9FKBS;	
		AC Q9FKBS;	
		DT 01-MAR-2001 (TREMBLrel. 16, Created)	
		DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	
		DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)	
		DE Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6	
		DE (Cyclin-dependent kinase inhibitor 3).	
		GN Name=rp3;	
		OS Arabidopsis thaliana (Mouse-ear cress).	
		OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;	
		OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
		NCBI_TaxID=3702;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RX MEDLINE-98403884; PubMed=9734815;	
		RX	

RA	Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N., Tabata S.	Qy	2 LXGRYEW 8
RT	"Structural analysis of Arabidopsis thaliana chromosome 5: VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned PI and TAC clones."	Db	152 LEGRYEW 158
RR	RN Res. 5:203-216(1998).		
RL	[2]		
SEQUENCE FROM N.A.		RESULT 4	
RX MEDLINE-21342510;	PubMed=11449057;	Q6T2Z0	PRELIMINARY;
RA de Veylder L., Beckman T., Beemster G.T.S., Kröls L., Terras F., Landriu I., Van Der Schueren E., Maes S., Naudts M., Inze D.; "Functional analysis of Cyclin-dependent kinase inhibitors of Arabidopsis"; Plant Cell 13:1653-1668(2001).	AC Q6T2Z0; ID Q6T2Z0; DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	AC Q6T2Z0; ID Q6T2Z0; DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	PRT; 166 AA.
RT EMBL; AB012242; BAB09435.1; -;	DR GO; GO:0005634; CAC41617.1; -;	DR GO; GO:0004861; P:cell cycle arrest; IEA.	DR GO; GO:0005634; C: nucleus; IEA.
RL EMBL; AU301534; CAC41617.1; -;	DR GO; GO:0007050; P:cell cycle arrest; CDI.	DR InterPro; IPR003175; CDI.	DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.	DR GO; GO:0006301; P:kinase activity; IEA.	DR GO; GO:0006301; P:kinase activity; IEA.	DR GO; GO:0006301; P:kinase activity; IEA.
KW Cyclin Kinase.	SEQUENCE 222 AA; 24925 MW; 7A3EB2C9A29688A7 CRC64;	DR GO; GO:0006301; P:kinase activity; IEA.	DR GO; GO:0006301; P:kinase activity; IEA.
SQ	Query Match 95.0%; Score 38; DB 2; Length 222; Best Local Similarity 85.7%; Pred. No. 14; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DR InterPro; IPR003175; CDI.	DR InterPro; IPR003175; CDI.
Qy 2 LXGRYEW 8	SQ	DR InterPro; IPR003175; CDI.	DR InterPro; IPR003175; CDI.
Db 211 LSGRYEW 217	Query Match 92.5%; Score 37; DB 2; Length 166; Best Local Similarity 85.7%; Pred. No. 17; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	DR GO; GO:0006301; P:kinase activity; IEA.	DR GO; GO:0006301; P:kinase activity; IEA.
RESULT 3	Q93V92 PRELIMINARY; PRT; 163 AA.	Qy 2 LXGRYEW 8	DR GO; GO:0006301; P:kinase activity; IEA.
AC Q93V92	AC Q93V92	Db 157 LEGRYEW 163	DR InterPro; IPR003175; CDI.
DT 01-DEC-2001 (TREMBLrel. 19, Created)	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		DR InterPro; IPR003175; CDI.
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	DE CDK/cyclin inhibitor. Name=Kikisla; Synonyms=Kikisla; Nicotiana tomentosiformis (Tobacco).		DR InterPro; IPR003175; CDI.
DE CDK/cyclin inhibitor. Name=Kikisla; Synonyms=Kikisla; Nicotiana tomentosiformis (Tobacco).	OS Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.		DR InterPro; IPR003175; CDI.
GN Nicotiana tomentosiformis (Tobacco).	OC		DR InterPro; IPR003175; CDI.
RR Jasinowski S., Perennec C., Bergounioux C., Glab N.; "Comparative Molecular and Functional Analyses of the Tobacco Cyclin-dependent kinase inhibitor NtKIS1B and its spliced variant NtKIS1B"; Plant Physiol. 130:1871-1882(2002).	OC		DR InterPro; IPR003175; CDI.
RN [2]	RR		DR InterPro; IPR003175; CDI.
SEQUENCE FROM N.A.	RR		DR InterPro; IPR003175; CDI.
RX MEDLINE-22169088; PubMed=12481070;	RR		DR InterPro; IPR003175; CDI.
RA Grondard S.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.	RR		DR InterPro; IPR003175; CDI.
RL EMBL; AU297906; CAC8733.1; -;	RR		DR InterPro; IPR003175; CDI.
DR EMBL; AU297904; CAC8733.1; -;	RR		DR InterPro; IPR003175; CDI.
DR GO; GO:0005634; C:nucleus; IEA.	RR		DR InterPro; IPR003175; CDI.
DR GO; GO:0004861; P:cell cycle arrest; IEA.	RR		DR InterPro; IPR003175; CDI.
DR GO; GO:0007050; P:cell cycle arrest; IEA.	RR		DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.	RR		DR InterPro; IPR003175; CDI.
KW SEQUENCE 163 AA; 18301 MW; E154A59D491B66B7 CRC64;	RR		DR InterPro; IPR003175; CDI.
Qy 92.5%; Score 37; DB 2; Length 163; Best Local Similarity 85.7%; Pred. No. 17; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	RR		DR InterPro; IPR003175; CDI.
Db 157 LEGRYEW 163	RR		DR InterPro; IPR003175; CDI.
RESULT 6	Q6T2Z1		DR InterPro; IPR003175; CDI.

Q6T2Z1 PRELIMINARY; PRT; 180 AA.
 Q6T2Z1; 05-JUL-2004 (TREMBrel. 27, Created)
 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 Cyclin-dependent kinase inhibitor 2,1 (Fragment).
 Glycine max (Soybean). Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 eurosids II; Brassicales; Brassicaceae; Arabidopsis;
 NCBI_TaxID=3847; [1]
 SEQUENCE FROM N.A.
 Li S., Reveratto S., Nielsen N.C.;
 Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 EMBL; AY39103; ASN13376.1;
 GO; GO:0016101; F:kinase activity; IEA.
 DR InterPro; IPR003175; CDI.
 Pfam; PF02234; CDI; 1.
 Cyclin Kinase.
 NON TER 180 20060 MW; 9E4ABB0918246E7 CRC64;
 SEQUENCE 180 AA; 20060 MW; 9E4ABB0918246E7 CRC64;
 Query Match 92.5%; Score 37; DB 2; Length 180;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Dy 2 LXGRYEW 8
 Db 171 LEGRYEW 177

RESULT 7
 Q6T2Z1 ASN13376 PRELIMINARY; PRT; 180 AA.
 ASN13376; AC
 ID DT 10-MAY-2004 (TREMBrel. 27, Created)
 AA13377; DT 10-MAY-2004 (TREMBrel. 27, Last sequence update)
 "Cyclin-dependent kinase inhibitor 2,1 (Fragment).
 Glycine max (Soybean). Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 eurosids II; Fabales; Papilionoideae; Phaseoleae; Glycine.
 NCBI_TaxID=3847; [1]
 SEQUENCE FROM N.A.
 Li S., Reveratto S., Nielsen N.C.;
 "CDNA of cell-cycle genes in soybean cetyl-dions";
 Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 EMBL; AY39103; ASN13376.1;
 Cyclin Kinase.
 NON TER 180 20060 MW; 9E4ABB0918246E7 CRC64;
 SEQUENCE 180 AA; 20060 MW; 9E4ABB0918246E7 CRC64;
 Query Match 92.5%; Score 37; DB 2; Length 180;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 171 LEGRYEW 177

RESULT 8
 Q6T2Z1 004154 PRELIMINARY; PRT; 191 AA.
 004154; AC
 ID DT 01-JUL-1997 (TREMBrel. 04, Created)
 01-JUL-1997 (TREMBrel. 04, Last sequence update)
 01-JUN-2003 (TREMBrel. 24, Last annotation update)
 Cyclin-dependent kinase inhibitor protein.
 NCBI_TaxID=3702; [1]
 SEQUENCE FROM N.A.
 RA RC RX RA
 Rounseley S.D., Kaul S.; Lin X., Ketchum K.A., Crosby M.L.,
 Wang H., Schorr P., Cutler A.J., Crosby L.C., Powke L.C.,
 "ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis
 thaliana interacts with both Cdc2a and Cyc33, and its expression is
 induced by abscisic acid.";
 Plant J. 15:501-510(1998).
 RL RN [2]
 SEQUENCE FROM N.A.
 RA RC RX RA
 Rounseley S.D., Kaul S.; Town C.D., Town C.D.,
 Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AF01958; AAC03040; AF01958; AAC03040;
 Somerville C.R., Somerville C.R., Venter J.C., Venter J.C.,
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL RN [3]
 SEQUENCE FROM N.A.
 RA RC RX RA
 Rounseley S.D., Kaul S.; Town C.D., Town C.D.,
 Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AF01958; AAC03040; AF01958; AAC03040;
 PIR: T01132; T01132;
 DR DR DR DR DR
 GO; GO:0005634; C:nucleus; IEA.
 GO; GO:0016301; F:kinase activity; IEA.
 GO; GO:0007050; P:cell cycle arrest; IEA.
 InterPro; IPR03175; CDI; 1.
 Pfam; PF02234; CDI; 1.

"Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [4]

INTERACTION WITH NUP50, AND MUTAGENESIS.
 RP MEDLINE=20271857; PubMed=10811608;
 RX Mueller D., Thieke K., Buerger A., Dickmanns A., Eilers M.;
 RT "Cyclin E-mediated elimination of p27 requires its interaction with
 the nuclear pore-associated protein mNUP60";
 RL EMBO J. 19:2168-2180(2000);
 CC FUNCTION: Involved in G1 arrest. May mediate TGF beta-induced G1
 arrest. Binds to and inhibits complexes formed by cyclin E-CDK2,
 cyclin A-CDK2, and cyclin D1-CDK4. Interaction with nucleoporin
 NUP50 is required for nuclear import and for degradation of
 phosphorylated p27kip1 after nuclear import.
 CC -!- SUBUNIT: Interacts with NUP50.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the CDI family.
 CC

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DR AA0440; AA21149.1; -.
 DR EMBL; U09968; AA20231.1; -.
 DR EMBL; BC014296; AAH14296.1; -.
 DR HSSP; P46522; 1sSU.
 DR MGI; MGI:104565; Cdkrab.
 DR GO; GO:0004861; F:cyclin-dependent protein binding; IPI.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007050; P:cell cycle arrest; IDA.
 DR GO; GO:0045736; P:negative regulation of CDK activity; IDA.
 DR InterPro; IPR003175; CDI.
 DR PF00234; CDI; 1.
 KW Cell cycle; Nuclear protein; Protein kinase inhibitor.
 FT DOMAIN 153 169 Nuclear localization signal (Potential).
 FT MUTAGEN 90 90 R>G; Loss of interaction with NUP50.
 SEQUENCE 197 AA; 2D19aCFF6EA650 CRC64;

Query Match 92.5%; Score 37; DB 1; Length 197;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 LXGRYEW 8
 | |||||
 Db 70 LEGRYEW 76

RESULT 14
 035792 PRELIMINARY; PRT; 197 AA.
 ID 035792
 AC 035792;
 DT 01-JAN-1998 (TREMBLrel 05, Created)
 DT 01-JAN-1998 (TREMBLrel 05, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel 24, Last annotation update)
 DB P27.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 STRAIN=Sprague-Dawley; TISSUE=Spleen;
 RX MEDLINE=9336761; PubMed=9218722;
 RA Nomura H., Sawada Y., Fujinaga K., Ohtaki S.;
 RT "Cloning and characterization of rat p27kip1, a cyclin-dependent
 kinase inhibitor";
 RL Gene 191:211-218(1997)
 DR EMBL; D83792; BAA21561.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . ; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 SQ .SEQUENCE 197 AA; 2D112 MW; 55738078C2D55B2 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 197;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 LXGRYEW 8
 | |||||
 Qy 70 LEGRYEW 76

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 55.7692 Seconds
 (without alignments)
 6.324 Million cell updates/sec

Title: US-09-574-735C-36

Perfect score: 3.2

Sequence: 1 EBXFFXXXE 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 35879299 residues

Total number of hits satisfying chosen parameters:

2002273

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_23Seq04:
 1: GeneseqD1900S:
 2: GeneseqD1900S:
 3: GeneseqD2000S:
 4: GeneseqD2001S:
 5: GeneseqD2002S:
 6: GeneseqD2003As:
 7: GeneseqD2003Bs:
 8: GeneseqD2004S:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	26	81.2	10	5	ABG65743	Plant ICK
2	26	81.2	10	5	ABG65738	Plant ICK
3	26	81.2	10	5	ABG65737	Plant ICK
4	26	81.2	87	5	ABG65672	OSICK 3 P
5	26	81.2	108	5	ABG65676	Bromo cor
6	26	81.2	262	5	ABG65670	ABG65670 OSICK 2 P
7	25	78.1	10	5	ABG65733	Plant ICK
8	25	78.1	10	5	ABG65739	Plant ICK
9	25	78.1	46	3	AAB26246	Rice cycl
10	25	78.1	46	3	AAP01941	Rice Cycl
11	25	78.1	60	3	AAP01953	Cyclin de
12	25	78.1	60	3	AAB2755	Soybean C
13	25	78.1	90	5	ABG65675	Rice Os I
14	25	78.1	99	3	AAB2751	Rice cycl
15	25	78.1	99	3	AAP01949	Cyclin de
16	25	78.1	194	5	ABG65691	Rice OSIC
17	25	78.1	205	3	AAP01952	Cyclin de
18	25	78.1	205	3	AAB2754	Soybean C
19	25	78.1	312	5	ABP28321	Streptoc
20	25	78.1	436	5	ABP30085	Streptoco
21	24	75.0	10	5	ABG65736	Plant ICK
22	24	75.0	10	5	ABG65731	Plant ICK
23	24	75.0	53	5	ABG65677	Lobolily
24	24	75.0	87	3	AAP01951	Cyclin de
25	24	75.0	87	3	AAB2753	Soybean C

This invention relates to the DNA and protein sequences of novel isolated (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficiency or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production of ICK inhibitors.

Disclosure; Page 14; 141pp; English.
 This invention relates to the DNA and protein sequences of novel isolated (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of the invention may be used for treating disorders characterised by insufficiency or excessive production of an ICK inhibitor. The protein of the invention may also be used to screen for naturally-occurring ICK substrates, drugs or compounds which modulate ICK activity, as well as to treat disorders characterised by insufficient or excessive production of ICK protein, forms which have decreased or aberrant activity compared to ICK wild type protein. The present sequence represents an inhibitor of cyclin dependent kinase (ICK) protein of the invention

XX

SQ	Sequence 10 AA;	Score 26; DB 5; Length 10;	AC	ABG65737;
Query Match	Best Local Similarity 81.2%; Pred. No. 7.7%; Mismatches 0; Indels 0; Gaps 0;	DT	27-AUG-2002 (first entry)	
Best Local Similarity 50.0%; Pred. No. 7.7%; Mismatches 5; Indels 5; Gaps 0;	XX	Plant ICK protein conserved motif 1 #45.		
Matches 5;	XX	DE		
Matches 5;	XX	KW		
Matches 5;	XX	XX		
Qy	1 EXEXFFXXE 10	OS	Plant; inhibitor of cyclin dependent kinase; ICK.	
Db	1 EIEAFFAAAE 10	OS	Oryza sativa.	
	XX	OS		
RESULT 2	WO200228893-A2.	PN		
ABG65738	ABG65738 standard; Peptide; 10 AA.	XX		
ID	ABG65738	PD	11-APR-2002.	
XX	ABG65738;	XX		
AC		PP	29-JUN-2001; 2001WO-1B001492.	
XX		XX		
XX	27-AUG-2002 (first entry)	PR	14-JUL-2000; 2000US-0218471P.	
XX	Plant ICK protein conserved motif 1 #46.	PR	13-OCT-2000; 2000US-0241219P.	
DE		XX	(CROP-) CROPDFSIGN NV.	
XX		PA		
XX	Plant; inhibitor of cyclin dependent kinase; ICK.	XX		
KW		PI	Frankard VMS, Peres Botta AM, Droual A, Mironov V, Inze D;	
XX		PI	Hatzfeld Y;	
OS		XX	WPI; 2002-471311/50.	
Oryza sativa.		XX		
XX	WO200228893-A2.	DR		
PN		XX		
XX	PR 11-APR-2002.	PS		
XX	XX	XX	This invention relates to the DNA and protein sequences of novel isolated	
XX	29-JUN-2001; 2001WO-1B001492.	CC	CC (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of	
XX	PR 14-JUL-2000; 2000US-0218471P.	CC	the invention may be used for treating disorders characterised by	
XX	PR 13-OCT-2000; 2000US-0241219P.	CC	insufficient or excessive production of an ICK inhibitor. The protein of	
XX	(CROP-) CROPDFSIGN NV.	CC	CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of	
XX	Frankard VMS, Peres Botta AM, Droual A, Mironov V, Inze D;	CC	the invention may be used for treating disorders characterised by	
XX	XX	CC	insufficient or excessive production of an ICK inhibitor. The protein of	
XX	WPI; 2002-471311/50.	CC	CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of	
XX	XX	CC	the invention may also be used to screen for naturally-occurring ICK	
XX	(CROP-) CROPDFSIGN NV.	CC	substrates, drugs or compounds which modulate ICK activity, as well as to	
XX	XX	CC	treat disorders characterised by insufficient or excessive production of	
XX	PI Frankard VMS, Peres Botta AM, Droual A, Mironov V, Inze D;	CC	CC ICK protein forms which have decreased or aberrant activity compared to	
XX	PI Hatzfeld Y;	CC	CC ICK wild type protein. The present sequence represents an inhibitor of	
XX	XX	CC	CC cyclin dependent kinase (ICK) protein of the invention	
XX	XX	XX	XX Sequence 10 AA;	
PS	Disclosure; Page 14; 141pp; English.	Query Match	Score 81.2%; Score 26; DB 5; Length 10;	
PS		Best Local Similarity 50.0%; Pred. No. 7.7%; Mismatches 5; Indels 0; Gaps 0;	DB	
PS		AC	ABG65672;	
PS		AC	ABG65672;	
PS		AC	ABG65672	
PS		XX	27-AUG-2002 (first entry)	
PS		XX	OSICK 3 protein.	
PS		XX	XX Plant; inhibitor of cyclin dependent kinase; ICK.	
PS		XX	OS Oryza sativa.	
PS		XX	PN WO200228893-A2.	
PS		XX	PD 11-APR-2002.	
RESULT 3	1 EXEXFFXXE 10	Qy	1 EXEXFFXXE 10	
ABG65737	1 EIEAFFAAAE 10	Db	1 EIEAFFAAAE 10	
ID ABG65737 standard; peptide; 10 AA.				

XX
 PP 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CRODDESIGN NV.
 XX
 PI Frankard VMS, Pères Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 DR N-PSDB; ABK93956.
 XX
 PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterized by an insufficient or excessive production
 PT of ICK inhibitors.
 XX
 PS Claim 48; Example 5; 141pp; English.

XX
 This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 Sequence 108 AA;

Query	Match	Score 81.2%;	DB 5;	Length 108;
	Best Local Similarity	50.0%;	Pred. No. 86;	
	Matches	5;	Conservative	0;
			Mismatches	5;
			Indels	0;
			Gaps	0;

XX
 SQ ID ABG65670 standard; protein; 262 AA.
 XX
 AC ABG65670;
 XX
 DT 27-AUG-2002 (First entry)
 XX
 DE OsICK 2 protein.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX
 OS Oryza sativa.
 XX
 PN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PP 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CRODDESIGN NV.
 XX
 PI Frankard VMS, Pères Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 DR N-PSDB; ABK93958.
 XX
 PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterised by an insufficient or excessive production
 PT of ICK inhibitors.
 XX
 PS Claim 48; Fig 3; 141pp; English.

XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 Sequence 87 AA;

Query	Match	Score 81.2%;	DB 5;	Length 87;
	Best Local Similarity	50.0%;	Pred. No. 69;	
	Matches	5;	Conservative	0;
			Mismatches	5;
			Indels	0;
			Gaps	0;

XX
 SQ ID ABG65676 standard; protein; 108 AA.
 XX
 AC ABG65676;
 XX
 DT 27-AUG-2002 (First entry)
 XX
 DE Broom corn ICK protein.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX
 OS Sorghum bicolor.
 XX
 PN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PP 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CRODDESIGN NV.
 XX
 PI Frankard VMS, Pères Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 DR N-PSDB; ABK93958.
 XX
 PT Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
 PT to screen substrates, drugs or compounds which modulate ICK activity and
 PT treat disorders characterised by an insufficient or excessive production
 PT of ICK inhibitors.
 XX
 PS Claim 48; Fig 3; 141pp; English.

XX
 CC This invention relates to the DNA and protein sequences of novel isolated
 CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
 CC the invention may be used for treating disorders characterised by
 CC an ICK inhibitor. The protein of
 CC the invention may also be used to screen for naturally occurring ICK
 CC substrates, drugs or compounds which modulate ICK activity, as well as to
 CC treat disorders characterised by insufficient or excessive production of
 CC ICK protein, forms which have decreased or aberrant activity compared to
 CC ICK wild type protein. The present sequence represents an inhibitor of
 CC cyclin dependent kinase (ICK) protein of the invention
 XX
 Sequence 108 AA;

Query	Match	Score 81.2%;	DB 5;	Length 108;
	Best Local Similarity	50.0%;	Pred. No. 86;	
	Matches	5;	Conservative	0;
			Mismatches	5;
			Indels	0;
			Gaps	0;

XX
 SQ ID ABG65676 standard; protein; 262 AA.
 XX
 AC ABG65676;
 XX
 DT 27-AUG-2002 (First entry)
 XX
 DE OsICK 2 protein.
 XX
 KW Plant; inhibitor of cyclin dependent kinase; ICK.
 XX
 OS Oryza sativa.
 XX
 PN WO200228893-A2.
 XX
 PD 11-APR-2002.
 XX
 PP 29-JUN-2001; 2001WO-IB001492.
 XX
 PR 14-JUL-2000; 2000US-0218471P.
 PR 13-OCT-2000; 2000US-0241219P.
 XX
 PA (CROP-) CRODDESIGN NV.
 XX
 PI Frankard VMS, Pères Bota AM, Droual A, Mironov V, Inze D;
 PI Hatzfeld Y;
 XX
 DR WPI; 2002-471311/50.
 DR N-PSDB; ABK93956.

KW cell growth; herbicide.
 XX
 OS *Oryza sativa*.
 XX
 PN WO200060087-A2.
 XX
 PD 12-OCT-2000.
 XX
 PR 05-APR-2000; 2000WO-US009106.
 XX
 PR 07-APR-1999; 99US-0128192P.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Klein TM, Weng Z, Cahoon RE;
 XX
 DR 2000-679375/66.
 DR N-PSDB; AAN15277.
 XX
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX
 PS Claim 10; Page 40; 58pp; English.

Query Match 78.1%; Score 25; DB 3; Length 46;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.
 CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the rice CDKI clone rsr9n.pk003.g12 as described
 CC in the method of the invention

SQ Sequence 46 AA;

Query Match 78.1%; Score 25; DB 3; Length 46;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC The present sequence is the rice cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of
 CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms

SQ Sequence 46 AA;

Query Match 78.1%; Score 25; DB 3; Length 46;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Rice Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0117.h4.

Qy 1 EXEXFPXXXX 10
 Db 6 ELEAFFAAEE 15

RESULT 11
 ID AAP01953 standard; protein; 60 AA.
 XX
 AC AAP01953;
 XX
 DT 01-NOV-2001 (first entry)
 DE Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0117.h4.
 XX
 KW Glycine max.
 XX
 OS Glycine max.
 XX
 PN WO200060087-A2.

XX
 AC AAP01953;
 XX
 DT 12-OCT-2000.
 DE Cyclin dependent kinase inhibitor sequences, useful for identifying
 KW herbicides and plant growth inhibitors.

XX
 PR 06-APR-2000; 2000WO-US009106.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Klein TM, Weng Z, Cahoon RE;
 XX
 DR 2000-679375/66.
 DR N-PSDB; AAN15277.

XX
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.

XX
 PS Claim 10; Fig 1; 58pp; English.

CC The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic

SQ Sequence 46 AA;

Query Match 78.1%; Score 25; DB 3; Length 46;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CC The present sequence is the rice cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA
 CC library for sequences similar to those encoding the CDKI from *Chenopodium*
 CC *rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of
 CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms

SQ Sequence 46 AA;

Query Match 78.1%; Score 25; DB 3; Length 46;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Rice Cyclin dependent kinase inhibitor (CDKI) clone s12.pk0117.h4.

Qy 1 EXEXFPXXXX 10
 Db 6 ELEAFFAAEE 15

RESULT 10
 ID AAP01941 standard; protein; 46 AA.
 XX
 AC AAP01941;
 XX
 DT 01-NOV-2001 (first entry)
 DE Rice Cyclin dependent kinase inhibitor (CDKI) clone rsr9n.pk003.g12.
 XX
 KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;
 KW plant growth inhibitor.
 OS *Oryza sativa*.
 XX
 PN WO200060087-A2.
 XX
 PD 12-OCT-2000.
 PR 06-APR-2000; 2000WO-US009106.
 XX
 PR 07-APR-1999; 99US-0128192P.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Klein TM, Weng Z, Cahoon RE;
 XX
 DR 2000-679375/66.

XX
 PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.

XX
 PS Claim 10; Fig 1; 58pp; English.

CC The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic

acid sequence that encodes CDK1 or affects the level of CDK1 expression. The encoded protein can be used in a method for evaluating a compound for its ability to inhibit the activity of a CDK1. The inhibitors can be used as herbicides. They can also be used to inhibit plant growth. The polynucleotide sequences can be used in gene mapping and as genetic markers. The sequence is the soybean CDK1 clone s12.ph0117.h4 as described in the method of the invention.

XX Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

Sequence 60 AA;

Query Match 78.1%; Score 25; DB 3; Length 60;

Best Local Similarity 50.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10

Db 19 ELEDFAAAE 28

19 ELEDFAAAE 28

RESULT 13

ABG5673

standard; protein: 90 AA.

AC AC5673;

27-AUG-2002 (first entry)

XX XX

Rice Os ICK associated peptide.

XX Plant; inhibitor of cyclin dependent kinase; ICK.

OS Oryza sativa.

XX PN WO200228893-A2.

XX XX

11-APR-2002.

PD PD

29-JUN-2001; 2001WO-TB001492.

PF PF

14-JUL-2000; 2000US-0218471P.

PR PR

13-OCT-2000; 2000US-0241219P.

XX XX

(CROP-) CRODESIGN NV.

XX XX

Frankard VMS, Peres Botta AM, Drouai A,

PI Mironov V, Inze D;

PI Ratzfeld Y;

XX XX

WPI; 2002-471311/50.

XX XX

PT PT

Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used

to screen substrates, drugs or compounds which modulate ICK activity and

treat disorders characterized by an insufficient or excessive production

of ICK inhibitors.

XX XX

Claim 48; Disclosure; 141pp; English.

XX XX

PT PT

Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of

ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of

ICK the invention may be used for treating disorders characterised by

the invention may be used for the production of an ICK inhibitor. The protein of

the invention may also be used to screen for naturally occurring ICK

substrates, drugs or compounds which modulate ICK activity, as well as to

treat disorders characterised by insufficient or excessive production of

ICK protein, forms which have decreased or aberrant activity compared to

ICK wild type protein. The present sequence represents an inhibitor of

cyclin dependent kinase (ICK) protein of the invention.

XX XX

Sequence 90 AA;

XX XX

Query Match 78.1%; Score 25; DB 5; Length 90;

Best Local Similarity 50.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EXEXFXXXE 10

DB 50 ELEDFAAAE 59

XX XX

RESULT 14

AAB27251

ID AAB27251 standard; protein: 99 AA.

AC AC

AAB27251;

17-JAN-2001 (first entry)

XX XX

Rice cyclin-dependent kinase inhibitor #2.

KW KW

XX cell growth; herbicide.
 XX Oryza sativa.
 XX WO200060087-A2.
 XX PD 12-OCT-2000.
 XX PP 06-APR-2000; 2000WO-US009106.
 XX PR 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PA Klein TM, Weng Z, Cahoon RE;
 XX PI Klein TM, Weng Z, Cahoon RE;
 XX DR WPI; 2000-679375/66.
 DR N-PSDB; AA95285.
 XX PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.
 XX PS Claim 10; Fig 1; 58pp; English.

XX The present sequence is the rice cyclin-dependent kinase inhibitor
 CC (CDKI). Its coding sequence was isolated by searching a rice leaf cDNA
 CC library for sequences similar to those encoding the CDKI from Chenopodium
 CC rubrum, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI is involved
 CC in the cell cycle, and may promote or inhibit cell division and growth.
 CC The protein and its coding sequence are useful in the production of
 CC transgenic plants which produce increased or decreased amounts of the
 CC CDKI protein, in the identification of herbicides, in genetic and
 CC physical mapping and in the isolation of the CDKI gene in other organisms
 XX Sequence 99 AA;

SQ

Query Match Score 25; DB 3; Length 99;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFFXXE 10
 Db 59 ELEAFFAAEE 68

RESULT 15

AAP01949 AAP01949 standard; protein; 99 AA.
 XX ID AAP01949
 XX AC AAP01949;
 XX DT 01-NOV-2001 (first entry)
 XX DB Cyclin dependent kinase inhibitor (CDKI) clone rsrn.pk003.g12:fs.
 XX KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; rice;
 KW plant growth inhibitor.
 XX OS Oryza sativa.
 XX PN WO200060087-A2.
 XX PR 07-APR-1999; 99US-0128192P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PA Klein TM, Weng Z, Cahoon RE;
 XX PI

XX PS Claim 10; Fig 1; 58pp; English.
 XX The invention describes a novel isolated polynucleotide comprising a
 CC specific cyclin dependent kinase
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitors (CDKIs) peptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 acid sequence that encodes CDKI or affects the level of CDKI expression.
 CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence is the rice CDKI clone rsrn.pk003.g12:fs as
 CC described in the method of the invention
 XX Sequence 99 AA;

SQ

Query	Match	Score	DB	Length
		78.1%	25	99;
		Best Local Similarity	50.0%	
		Matches	5	
		Conservative	0	
		Mismatches	5	
		Indels	0	
		Gaps	0	

Qy 1 EXEXFFXXE 10
 Db 59 ELEAFFAAEE 68

Search completed: October 26, 2004, 15:36:54
 Job time : 57.7692 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:19:44 ; Search time 16.5385 Seconds
 (without alignments)
 40.099 Million cell updates/sec

Title: US-09-574-735C-36
 Perfect score: 3.2
 Sequence: 1 EXEFFXXXXE 10
 Scoring Table: BLOSUM62
 Gappen 10.0 , Gapext 0.5
 Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgn2_6/picodata/1/iaa/5A-COMB.PEP:
 2: /cgn2_6/picodata/1/iaa/5B-COMB.PEP:
 3: /cgn2_6/picodata/1/iaa/6A-COMB.PEP:
 4: /cgn2_6/picodata/1/iaa/6B-COMB.PEP:
 5: /cgn2_6/picodata/1/iaa/PCTUS-COMB.PEP:
 6: /cgn2_6/picodata/1/iaa/backfile1.DEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	75.0	222	4 US-09-574-735C-4	Sequence 4, Appli
2	23	75.0	583	3 US-09-311-311C-24	Sequence 24, Appli
3	23	71.9	117	4 US-09-107-532A-6482	Sequence 6482, Appli
4	23	71.9	117	4 US-09-134-000C-6761	Sequence 5761, Appli
5	23	71.9	117	4 US-09-134-000C-6140	Sequence 6140, Appli
6	23	71.9	209	4 US-09-536-597D-2	Sequence 2, Appli
7	23	71.9	860	4 US-09-248-79A-1895	Sequence 1895, Appli
8	23	71.9	966	4 US-09-638-188B-154	Sequence 154, Appli
9	23	71.9	966	4 US-09-291-411D-154	Sequence 154, Appli
10	23	71.9	117	4 US-09-638-188B-107	Sequence 107, Appli
11	23	71.9	968	4 US-09-638-188B-155	Sequence 155, Appli
12	23	71.9	968	4 US-09-291-411D-107	Sequence 107, Appli
13	23	71.9	968	4 US-09-291-411D-155	Sequence 155, Appli
14	22	68.8	207	4 US-09-194-452A-1014	Sequence 1014, Appli
15	22	68.8	248	4 US-09-543-68A-7444	Sequence 7444, Appli
16	22	68.8	313	3 US-08-995-335-8	Sequence 8, Appli
17	22	68.8	313	3 US-09-410-372-8	Sequence 8, Appli
18	22	68.8	359	4 US-09-248-7962-25757	Sequence 25757, Appli
19	22	68.8	408	4 US-09-348-352A-4855	Sequence 4855, Appli
20	22	68.8	440	3 US-08-985-335-3	Sequence 3, Appli
21	22	68.8	440	3 US-09-410-372-3	Sequence 12, Appli
22	22	68.8	600	3 US-08-856-519-12	Sequence 7380, Appli
23	22	68.8	600	4 US-09-489-039A-7380	Sequence 9, Appli
24	22	68.8	615	3 US-09-297-937C-9	Sequence 1, Appli
25	22	68.8	694	3 US-09-440-322A-1	Sequence 1, Appli
26	22	694	4 US-09-846-998A-1	Sequence 1, Appli	
27	22	68.8	722	4 US-09-105-058C-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1
 US-09-546-597D-4
 ; Sequence 4, Application US/09526597D
 ; Patent No. 6710227
 ; GENERAL INFORMATION:
 ; APPLICANT: De Veylder, Lieven
 ; APPLICANT: De Almeida, Janice
 ; APPLICANT: Landrieu, Isabelle
 ; FILE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
 ; FILE REFERENCE: 1187-2
 ; CURRENT APPLICATION NUMBER: US/09/526-597D
 ; CURRENT FILING DATE: 2000-03-16
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 4
 ; LENGTH: 222
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-09-526-597D-4

Query Match 1 EXEFFXXXXE 10
 Best Local Similarity 75.0%; Score 24; DB 4; Length 222;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy Db 181 EMEREFPAAE 190

RESULT 2
 US-09-311-311C-24
 ; Sequence 24, Application US/09311311C
 ; Patent No. 6358378
 ; GENERAL INFORMATION:
 ; APPLICANT: Brison, et al.
 ; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
 ; TITLE OF INVENTION: METHODS, AND USES THEREFOR
 ; FILE REFERENCE: 1874-117
 ; CURRENT APPLICATION NUMBER: US/09/311,311C
 ; CURRENT FILING DATE: 1999-05-13
 ; PRIOR APPLICATION NUMBER: US 60/085,296
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO: 24
 ; LENGTH: 583
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE: CHAIN
 ; NAME/KEY: CHAIN

LOCATION: {1}..:(583)
 OTHER INFORMATION: GRASP65 protein
 US-09-311-311C-24

Query Match Score 24; DB 3; Length 583;
 Best Local Similarity 50.0%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10
 Db 144 ESEDEFTLIE 153

RESULT 3
 US-09-107-512A-6482
 Sequence 6482, Application US/09107532A
 Patent No. 6581275

GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 73:10

CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02354

COMPUTER READABLE FORM:
 COMPUTER: PC
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: JULY 2, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 6482:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1..117
 SEQUENCE DESCRIPTION: SEQ ID NO: 6482:
 US-09-107-512A-6482

Query Match Score 23; DB 4; Length 117;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10
 Db 65 EEEESFFMVMVE 74

RESULT 4
 US-09-134-000C-5761
 Sequence 5761, Application US/09134000C
 Patent No. 6617156

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: 60/055,778

PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 5761
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-5761

Query Match Score 23; DB 4; Length 117;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10
 Db 65 EEEESFFMVMVE 74

RESULT 5
 US-09-134-000C-6140
 Sequence 6140, Application US/09134000C
 Patent No. 6617156

GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 6140
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-6140

Query Match Score 23; DB 4; Length 117;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXE 10
 Db 65 EEEESFFMVMVE 74

RESULT 6
 US-09-526-597D-2
 Sequence 2, Application US/09526597D
 Patent No. 6710227

GENERAL INFORMATION:
 APPLICANT: De Veylder, Lieven
 APPLICANT: De Almeida, Janice
 APPLICANT: Landrieu, Isabelle
 TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof

CURRENT APPLICATION NUMBER: US/09/526,597D
 CURRENT FILING DATE: 2000-03-16
 NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-2

Query Match Score 23; DB 4; Length 209;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
Db 164 ELEDFFOVAE 173

RESULT 9
US-09-291-417D-154
; Sequence 154, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 154
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-154

Query Match Score 23; DB 4; Length 966;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
Db 933 EQEMFFKLSE 942

RESULT 10
US-09-688-188B-107
; Sequence 107, Application US/09688188B
; Patent No. 6656216
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 107
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-107

Query Match Score 23; DB 4; Length 968;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
Db 934 EQEMFFKLSE 943

RESULT 11
US-09-688-188B-154
; Sequence 154, Application US/09688188B
; Patent No. 6656216
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 154
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-688-188B-154

Query Match Score 23; DB 4; Length 966;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;

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; Sequence 155, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION: PLOWMAN, GREGORY
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 155
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-155

RESULT 12
US-09-291-417D-107
Sequence 107, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION: PLOWMAN, GREGORY
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 107
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-107

Query Match 71.9%; Score 23; DB 4; Length 968;
Best Local Similarity 50.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 EXEXFXXXE 10
Db 934 EQEMFFKLSE 943

RESULT 13
US-09-291-417D-155
Sequence 155, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION: PLOWMAN, GREGORY
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 107
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-291-417D-155

Query Match 71.9%; Score 23; DB 4; Length 968;
Best Local Similarity 50.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 EXEXFXXXE 10
Db 934 EQEMFFKLSE 943

RESULT 14
US-09-198-452A-1014
Sequence 1014, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION: PLOWMAN, GREGORY
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments and treatment of infection
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO: 1014
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1014

Query Match 68.8%; Score 22; DB 4; Length 207;
Best Local Similarity 66.7%; Pred. No. 4.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EXEXPF 6
Db 123 EAETFF 128

RESULT 15
US-09-543-681A-7484
Sequence 7484, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION: PLOWMAN, GREGORY
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 7484
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7484

Query Match 68.8%; Score 22; DB 4; Length 248;
Best Local Similarity 66.7%; Pred. No. 5.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EXEXPF 6

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Db 128 ESEAFF 133

Search completed: October 26, 2004, 15:34:20
Job time : 17.5385 secs



RESULT 2
 US-10-333-006-16
 ; Sequence 16, Application US/103333006
 ; Publication No. US20040019926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1le S.
 ; APPLICANT: Peres Bota, Adrian Marius
 ; APPLICANT: Droual, Anne-Marie
 ; APPLICANT: Mironov, Vladimir
 ; APPLICANT: Inz, Dirk
 ; APPLICANT: Hatzfeld, Yves
 ; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
 ; FILE REFERENCE: 1187-13
 ; CURRENT APPLICATION NUMBER: US/10/333,006
 ; CURRENT FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01492
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIORITY NUMBER: US 60/218,471
 ; PRIORITY NUMBER: US 60/218,471
 ; PRIORITY NUMBER: US 60/241,219
 ; PRIORITY NUMBER: US 60/241,219
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 16
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 US-10-333-006-16

Query Match 81.2%; Score 26; DB 15; Length 108;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02; Gaps 0;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 67 EIEAFFAAAE 76

RESULT 3
 US-10-437-963-198574
 ; Sequence 198574, Application US/10437963
 ; Publication No. US/040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Ross, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbuzuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 198574
 ; LENGTH: 225
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9421C.1.pep

Query Match 81.2%; Score 26; DB 16; Length 225;
 Best Local Similarity 50.0%; Pred. No. 2.5e+02; Gaps 0;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10

RESULT 4
 US-10-333-006-10
 ; Sequence 10, Application US/10333006
 ; Publication No. US20040019926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frankard, Valerie Marie-No. US20040019926A1le S.
 ; APPLICANT: Peres Bota, Adrian Marius
 ; APPLICANT: Droual, Anne-Marie
 ; APPLICANT: Mironov, Vladimir
 ; APPLICANT: Inz, Dirk
 ; APPLICANT: Hatzfeld, Yves
 ; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS
 ; FILE REFERENCE: 1187-13
 ; CURRENT APPLICATION NUMBER: US/10/333,006
 ; CURRENT FILING DATE: 2003-01-14
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01492
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIORITY NUMBER: US 60/218,471
 ; PRIORITY NUMBER: US 60/241,219
 ; PRIORITY NUMBER: US 60/241,219
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 10
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-333-006-10

Query Match 81.2%; Score 26; DB 15; Length 262;
 Best Local Similarity 50.0%; Pred. No. 2.9e+02; Gaps 0;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 217 EIEAFFAAAE 226

RESULT 5
 US-10-437-963-195115
 ; Sequence 195115, Application US/10437963
 ; Publication No. US/040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Ross, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbuzuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 195115
 ; LENGTH: 417
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE: FEATUR
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_91095C.1.pep

Query Match 81.2%; Score 26; DB 16; Length 417;
 Best Local Similarity 50.0%; Pred. No. 4.6e+02; Gaps 0;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10

Db 372 EIEAFFAAE 381

RESULT 8

US-10-333-006-44

; Sequence 44, Application US/10333006

; Publication No. US20040019926A1

; GENERAL INFORMATION:

; APPLICANT: Frankard, Valerie Marie-No.

US20040019926A1le S.

; APPLICANT: Droual, Anne-Marie

Marius

; APPLICANT: Mironov, Vladimir

Inz, Dirk

Hatzfeld, Yves

; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS

; FILE REFERENCE: 1187-13

; CURRENT APPLICATION NUMBER: US/10/333,006

; CURRENT FILING DATE: 2003-01-14

; PRIOR APPLICATION NUMBER: PCT/IB01/01492

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/218,471

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/241,219

; PRIOR FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 13

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-333-006-13

Query Match 78.1%; Score 25; DB 15; Length 94;
Best Local Similarity 50.0%; Pred. No. 3.e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0;
Gaps 0;

Qy 1 EXEXFFXXXX 10
Db 50 EIEAFFAAE 59

RESULT 9

US-10-437-963-120870

; Sequence 120870, Application US/10437963

; GENERAL INFORMATION:

; Publication No. US20040123343A1

; APPLICANT: La Rosa, Thomas J.

Kovalic, David K.

Zhou, Yihua

Cao, Yongwei

Wu, Wei

Bokharov, Andrey A.

Babarazuk, Brad

Ping, Li

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(5321)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO: 120870

; LENGTH: 194

; TYPE: PRT

; ORGANISM: Oryza sativa

; OTHER INFORMATION: Clone ID: PAT_MRT4530_23950C.1.pep

US-10-437-963-120870

Query Match 78.1%; Score 25; DB 16; Length 194;
Best Local Similarity 50.0%; Pred. No. 3.e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0;
Gaps 0;

Qy 1 EXEXFFXXXX 10
Db 54 EMBEBFSAAE 63

RESULT 6

US-10-333-006-13

; Sequence 13, Application US/10333006

; Publication No. US20040019926A1

; GENERAL INFORMATION:

; APPLICANT: Frankard, Valerie Marie-No.

US20040019926A1le S.

; APPLICANT: Droual, Anne-Marie

Marius

; APPLICANT: Mironov, Vladimir

Inz, Dirk

Hatzfeld, Yves

; TITLE OF INVENTION: NOVEL PLANT CYCLIN-DEPENDENT KINASE INHIBITORS

; FILE REFERENCE: 1187-13

; CURRENT APPLICATION NUMBER: US/10/333,006

; CURRENT FILING DATE: 2003-01-14

; PRIOR APPLICATION NUMBER: PCT/IB01/01492

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/218,471

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/241,219

; PRIOR FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 13

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-333-006-13

Query Match 78.1%; Score 25; DB 16; Length 95;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0;
Gaps 0;

Qy 1 EXEXFFXXXX 10
Db 54 EMBEBFSAAE 63

RESULT 10
US-10-434-599-182928
; Sequence 182928, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182928
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1.pep
US-10-424-599-182928

Qy	1 EXEXFFXXE 10
Db	164 EIEEFFRAAE 173

Query Match Score 78.1%; Best Local Similarity 50.0%; Matches 5; Conservative 0; Pred. No. 3.9e+02; Indels 0; Gaps 0;

RESULT 11
US-10-437-963-128205
; Sequence 128205, Application US/10437963
; Publication No. US20040123333A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barboza, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128205
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(21B)
; OTHER INFORMATION: unsure at all Xaa locations

Qy	1 EXEXFFXXE 10
Db	180 EXEEFPAAAE 189

Query Match Score 78.1%; Best Local Similarity 60.0%; Matches 6; Conservative 0; Pred. No. 4.1e+02; Indels 4; Gaps 0;

RESULT 12
US-10-425-114-59718
; Sequence 59718, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59718
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3732-047-G6_FLI.pep
US-10-425-114-59718

Qy	1 EXEXFFXXE 10
Db	207 EMEBFPSAAE 216

Query Match Score 78.1%; Best Local Similarity 50.0%; Matches 5; Conservative 0; Pred. No. 4.7e+02; Indels 5; Gaps 0;

RESULT 13
US-10-425-114-61054
; Sequence 61054, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61054
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3279-047-A7_FLI.pep
US-10-425-114-61054

Qy	1 EXEXFFXXE 10
Db	214 EMEBFPSAAE 223

Query Match Score 78.1%; Best Local Similarity 50.0%; Matches 5; Conservative 0; Pred. No. 4.8e+02; Indels 5; Gaps 0;

RESULT 14
US-10-369-493-22727
; Sequence 22727, Application US/10369493
; Publication No. US2003023365A1
; GENERAL INFORMATION:

```

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10152052.B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIORITY NUMBER: US 60/360,039
; PRIORITY FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 22727
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .(401)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-22727

Query Match          78.1%;   Score 25;  DB 14;  Length 401;
Best Local Similarity      50.0%; Pred. No. 7.5e+02;
Matches      0;  Mismatches 5;  Indels 0;  Gaps 0;

Qy          1 EXEFFFFXXE 10
          ||| |
Db          351 ETESFFQAKE 360

RESULT 15
US-10-369-493-22728
; Sequence 22728, Application US/10369493
; Publication No. US2003033675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10152052.B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIORITY NUMBER: US 60/360,039
; PRIORITY FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 22728
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .(401)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-22728

Query Match          78.1%;   Score 25;  DB 14;  Length 401;
Best Local Similarity      50.0%; Pred. No. 7.5e+02;
Matches      0;  Mismatches 5;  Indels 0;  Gaps 0;

Qy          1 EXEFFFFXXE 10
          ||| |
Db          351 ETESFFQAKE 360

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A;Cross-references: EMBL:AL032824; PIDN:CAB37422.1; GSPDB:GN00068; SPDB:SPCC584.09
 A;Experimental source: strain 97lh-; cosmid c584
 R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 Submitted to the EMBL Data Library, November 1995

A;Reference number: Z1-1830

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Accession: T39129

A;Residues: 1-380 <LY2>

A;Cross-references: EMBL:Z66569; NID:g1052533; PIDN:CAA91517.1; PID:g1052538; SPDB:SPAC8
 C;Genetics: <LYN1>
 A;Gene: SPC188.12
 A;Map Position: 3
 A;Introns: 20/2
 C;Genetics: <SEE2>
 A;Gene: SPC184.09
 A;Map Position: 3
 A;Introns: 20/2
 C;Genetics: <LY23>
 A;Gene: SPDB:SPAC8A4.07
 A;Map position: 1
 A;Introns: 20/2
 C;Superfamily: Saccharomyces cerevisiae cell division control protein CDC10
 Query Match 78.1%; Score 25; DB 2; Length 380;
 Best Local Similarity 50.0%; Pred. No. 65;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 EXEXFXXXXE 10
 Db 330 ETESFFQAK 339

RESULT 3
 T02656
 Probable salt-inducible protein [imported] - Arabidopsis thaliana
 N;Alternate names: hypothetical protein F12C20.17
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: T02656; H84664
 R;Rounsley, S.D.; Roanning, C.W.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; SW
 submitted to the EMBL Data Library, August 1998
 A;Description: Arabidopsis thaliana Chromosome II BAC F12C20 genomic sequence.
 A;Reference number: Z14685
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-739 <ROJ>
 A;Cross-references: UNIPROT:OB1028; EMBL:AC005168; PID:93426046
 A;Experimental source: cultiver Columbia
 R;Lin, X.; Kaul, S.; Bounslie, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shan, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Niever, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Accession number: A84420; PMID:20083487; PMID:10617197
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-739 <STO>
 A;Cross-references: GB:AE002093; NID:93426046; PIDN: AAC32245.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: F12C20.17; At2g26790
 A;Map position: 2

Query Match 78.1%; Score 25; DB 2; Length 799;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 511 EAEDFSSLE 520

RESULT 4
 T09668
 cyclin-dependent kinase inhibitor protein - red goosefoot
 C;Species: Chenopodium rubrum (red goosefoot)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 R;Fountain, M.D.; Renz, A.; Beck, E.
 submitted to the EMBL Data Library, November 1997
 A;Description: A plant Gi cyclin-dependent kinase inhibitor gene from a photoautotrophic
 A;Reference: T09668
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-196 <FOU>
 A;Cross-references: UNIPROT:048597; EMBL:AJ002173
 A;Experimental source: photoautotrophic cells derived from hypocotyl tissue
 C;Genetics:
 A;Gene: CDK11
 A;Keywords: protein kinase inhibitor

Query Match 75.0%; Score 24; DB 2; Length 196;
 Best Local Similarity 50.0%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 155 EIEEFFAVAE 164

RESULT 5
 T15928
 hypothetical protein EEBD8.2 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Accession: T15928
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 R;Chissone, S.
 submitted to the EMBL Data Library, July 1995
 A;Description: The sequence of *C. elegans* cosmid EEBD8.
 A;Reference number: Z18428
 A;Accession: T15928
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-295 <CHI>
 A;Cross-references: UNIPROT:Q09529; EMBL:U23484; NID:9733597; PID:9733599; PIDN: AAC46762
 A;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CESPEEBD8.2
 A;Introns: 84/3; 13/3; 275/3

Query Match 75.0%; Score 24; DB 2; Length 299;
 Best Local Similarity 50.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 134 EEEESFFSLHE 143

RESULT 6
 C83945
 stage V sporulation protein K BH2363 [imported] - *Bacillus halodurans* (strain C-125)
 C;Species: *Bacillus halodurans*
 C;Accession: C83945
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650; PMID:20512582; PMID:11056132
 A;Accession: C83945
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-315 <STO>

A;Cross-references: UNIPROT:Q9WAC6; GB:AP001515; NID:910174886; PIDN:BA060
 A;Experimental source: strain C-125
 C;Generics:
 A;Gene: BH3363
 C;Superfamily: cfxQ protein

Query Match	75.0%;	Score 24;	DB 2;	Length 315;
Best Local Similarity	50.0%;	Pred. No.	96;	
Matches	5;	Conservative	0;	Mismatches
Qy	1 EXEXFXXXX 10	5;	Indels	0;
Db	26 EEEFFHSEE 35	0;	Gaps	0;

RESULT 7
 A81704
 DNA ligase TC0423 [imported] - Chlamydia muridarum (strain Nigg)
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 12-Jul-2004
 C;Accession: A81704
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, R.C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res., 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; PMID:20150255; PMID:10684935
 A;Accession: A81704
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-660 <PEN>
 A;Cross-references: UNIPROT:Q9PKP2; GB:AP002309; NID:91190464; PIDN:AF03927

RESULT 10
 T04092
 phospholipase D (EC 3.1.4.4) - common tobacco
 C;Species: Nicotiana tabacum (common tobacco)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T04092
 R;Lein, W.; Saalbach, G.
 submitted to the EMBL Data Library, May 1997
 A;Description: Characterization of tobacco phospholipase D.
 A;Reference number: Z15203
 A;Accession: T04092
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-808 <LET>
 A;Cross-references: UNIPROT:P93400; EMBL:284822; NID:e1057206; PIDN:CAB06620.1; PID:e33

RESULT 8
 C11551
 Probable DNA ligase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
 C;Species: Chlamydia trachomatis
 C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 12-Jul-2004
 C;Accession: C11551
 R;Stephens, R.S.; Kallman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
 A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A;Reference number: AY1570; PMID:93000809; PMID:9714136
 A;Accession: C11551
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-663 <ARN>
 A;Cross-references: UNIPROT:O84148; GB:AE001288; GB:AE001273; NID:g3328545; PIDN: AAC6773

RESULT 11
 B81014
 hypothetical protein NNB2037 [imported] - Neisseria meningitidis (strain MC58 serogroup C)
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: B81014; F81956
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.J.; Hickman, B.K.; Huff, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Yamathavan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: B81014

A;Accession: A69950
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-146 <XDN>
A;Cross-references: UNIPROT:P45445; GB:Z99117; GB:AL009126; NID:92634966; PIDN:CAB14521.
A;Experimental source: strain 168
C;Genetics:
A;Gene: Yqck

Query	Match	71.9%	Score 23;	DB 2;	Length 146;
	Best Local Similarity	50.0%	Pred. No. 77;		
	Matches	5;	Conservative	0;	Mismatches
Db	Qy	1 EXXFFXXE 10		5;	Indels 0;
					Gaps 0;
		81 EKEGFFAREE 90			

Search completed: October 26, 2004, 15:40:10
Job time : 15.8462 secs



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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:27:03 ; Search time 55.7692 Seconds
(without alignments)
103.171 Million cell updates/sec

Title: US-09-574-735C-36
Perfect score: 32
Sequence: 1_EEEXFXXXE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	26	81.2	262	2	Q626G5	06z695 oryza sativa
2	26	81.2	262	2	BAD17213	Bad17213 oryza sat
3	25	78.1	62	2	C83503	083503 treponema p
4	25	78.1	166	2	Q67220	06t220 glycine max
5	25	78.1	166	2	AaS13377	Aas13377 glycine m
6	25	78.1	166	2	Q91ry0	Q91ry0 arabidopsis
7	25	78.1	192	2	Q9Ff28	Q9Ff28 pisum sativ
8	25	78.1	205	2	Q6t223	Q6t223 glycine max
9	25	78.1	205	2	AAS13374	Aas13374 glycine m
10	25	78.1	223	2	Q6LlB0	Q6LlB0 photobacter
11	25	78.1	223	2	CAG22039	CAG22039 photobact
12	25	78.1	242	2	Q7DH8	Q7xhd8 oryza sativ
13	25	78.1	242	2	Q9Fw65	Q9Fw65 oryza sativ
14	25	78.1	293	2	Q92rw5	Q92rw5 rhizobium m
15	25	78.1	380	1	SPN6_SCHPO	Q99883 schizosacch
16	25	78.1	436	2	QBDFV3	Q8dzv3 streptococc
17	25	78.1	436	2	QBESKL	Q8esk1 streptococc
18	25	78.1	618	2	Q7S542	Q7s542 neurospora
19	25	78.1	799	2	Q81028	Q81028 arabidopsis
20	24	75.0	123	2	Q6ZWH0	Q6zwh0 homo sapien
21	24	75.0	123	2	BACB5533	BacB5533 homo sapi
22	24	75.0	148	2	Q67567	Q67567 digitaria s
23	24	75.0	185	2	Q8GT28	Q8gt28 lycorensis
24	24	75.0	196	2	Q7RH53	Q7rh53 plasmoidium
25	24	75.0	196	2	C48597	C48597 chenopodium
26	24	75.0	198	2	Q6T222	Q6t222 glycine max
27	24	75.0	198	2	AAS13375	Aas13375 glycine m
28	24	75.0	210	2	Q8GT29	Q8gt29 lycorensis
29	24	75.0	222	2	Q9FB5	Q9fb5 arabidopsis
30	24	75.0	260	2	Q6CS15	Q6c915 yarrowia li
31	24	75.0	264	2	Q7U204	Q7u204 leptospira

ALIGNMENTS

RESULT 1									
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DT	05-JUL-2004	{TREMBLIRE}	27,	Last sequence update)	DT	05-JUL-2004	{TREMBLIRE}	27,	Last sequence update)
DT	05-JUL-2004	{TREMBLIRE}	27,	Last annotation update)	DE	Hypothetical protein P0486G3.18			
GN	Name=P0486G03.18;				OS	Oryza sativa (Japonica cultivar-group);			
OC	Bukaryota; Viridiplante; Streptophytina; Embryophyta; Tracheophyta;				OC	Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Eukaryota; Viridiplante; Streptophytina; Embryophyta; Tracheophyta;				OX	Oryzeae; Oryza.			
NCBI_TaxID=393947;					DR	Pfam: PF02234; CDD: 1.			
RN					KW	Hypothetical protein;			
SEQUENCE FROM N.A.					SQ	SEQUENCE 262 AA;			
RA	Sasaki T., Matsumoto T., Yamamoto K.;				RP	SEQUENCE FROM N.A.			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				RA	Sasaki T., Matsumoto T., Yamamoto K.;			
DR	EMBL; AP005003; BAD1723.1; -.				DR	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	InterPro; IPR03175; CDI.				DR	InterPro; IPR03175; CDI.			
[1]	-				DR	NCBI_TaxID=393947;			
SEQUENCE FROM N.A.					DR	Pfam: PF02234; CDD: 1.			
RA	Sasaki T., Matsumoto T., Yamamoto K.;				DR	Hypothetical protein;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				DR	SEQUENCE 262 AA;			
DR	EMBL; AP005003; BAD1723.1; -.				DR	SEQUENCE FROM N.A.			
DR	InterPro; IPR03175; CDI.				DR	SEQUENCE FROM N.A.			
DR	NCBI_TaxID=393947;				DR	SEQUENCE FROM N.A.			
Query Match:					DR	SEQUENCE FROM N.A.			
Best Local Similarity					DR	SEQUENCE FROM N.A.			
Matches 5;					DR	SEQUENCE FROM N.A.			
Conservative 5;					DR	SEQUENCE FROM N.A.			
Mismatches 0;					DR	SEQUENCE FROM N.A.			
Indels 0;					DR	SEQUENCE FROM N.A.			
Gaps 0;					DR	SEQUENCE FROM N.A.			
Qy	1 EXEYFXXXX 10				DR	SEQUENCE FROM N.A.			
					DR	SEQUENCE FROM N.A.			
Db	217 EIEAFFAAAE 226				DR	SEQUENCE FROM N.A.			
RESULT 2					DR	SEQUENCE FROM N.A.			
ID	BAD17213	PRELIMINARY;	PRT;	262 AA.	DR	SEQUENCE FROM N.A.			
AC	BAD17213	PRELIMIRE;	27,	Created)	DR	SEQUENCE FROM N.A.			
DT	10-MAY-2004	{TREMBLIRE}	27,	Last sequence update)	DR	SEQUENCE FROM N.A.			
DT	10-MAY-2004	{TREMBLIRE}	27,	Last annotation update)	DR	SEQUENCE FROM N.A.			
GN	Name=P0486G3.18;				DR	SEQUENCE FROM N.A.			
OC	Oryza sativa (Japonica cultivar-group);				DR	SEQUENCE FROM N.A.			
OC	Bukaryota; Viridiplante; Streptophytina; Embryophyta; Tracheophyta;				DR	SEQUENCE FROM N.A.			
OC	Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;				DR	SEQUENCE FROM N.A.			
OC	Oryzeae; Oryza.				DR	SEQUENCE FROM N.A.			
NCBI_TaxID=393947;					DR	SEQUENCE FROM N.A.			
RN					DR	SEQUENCE FROM N.A.			
STRAIN=cv.					DR	SEQUENCE FROM N.A.			
RA	Sasaki T., Matsumoto T., Yamamoto K.;				DR	SEQUENCE FROM N.A.			
RT	"Oryza sativa nipponbare (GA3)" Genomic DNA, chromosome 2, PAC				DR	SEQUENCE FROM N.A.			
RT	clone:P0486G3.18."				DR	SEQUENCE FROM N.A.			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				DR	SEQUENCE FROM N.A.			

DR	EMBL; AP005002; BAD12213.1; -.		DR	InterPro; IPR003175; CDI.	
KW	Hypothetical Protein.		DR	Pram; PF0224; CDI; 1.	
SEQUENCE	262 AA; 27138 MW; 42EC85C8276C0726 CRC64;		KW	Cyclin Kinase.	
Query Match	81.2%; Score 26; DB 2; Length 262;		FT	NON TER 166 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;	
Best Local Similarity	50.0%; Pred. No. 1.4e+02;		SEQUENCE	166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;	
Matches	5; Conservative 5; Indels 0; Gaps 0; Mismatches 5; Score 25; DB 2; Length 166;		Query Match	78.1%; Score 25; DB 2; Length 166;	
Qy	1 EXEXFFXXXX 10		Best Local Similarity	50.0%; Pred. No. 1.6e+02; Mismatches 5; Conservative 5; Indels 0; Gaps 0;	
Db	217 EIEAFFAAAE 226		Qy	1 EXEXFFXXXX 10	
RESULT 3					
OS3503	PRELIMINARY;	PRT;	166 AA.	Db	127 ELEDFFAAAE 136
ID	083503;				
AC	AC083503;				
DT	01-NOV-1998 (TRMBLrel. 08; Created)				
DT	01-JUN-2003 (TRMBLrel. 08; Last sequence update)				
DT	01-JUN-2003 (TRMBLrel. 24; Last annotation update)				
DE	Hypothetical protein TP0490.				
GN	OrderedLocusName=TP0490;				
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.				
OX	NCBI_TaxID=160;				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=Nichols;				
RX	MEDLINE#9832770; PubMed=9665878;				
RA	Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G., Dodson R.J., Gwin-Mill, Hickey E.K., Clayton R.A., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D., Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M., Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M., Weidman J.P., Smith H.O., Venter J.C.; "Complete genome sequence of <i>Treponema pallidum</i> , the syphilis spirochete,"				
RT	Science 281:375-388(1998).				
RL	PMID: A001225; AAC65477.1; -.				
DR	PIR; B71318; B71318.				
DR	TIGR; TP0490; -.				
KW	Complete proteome; Hypothetical protein.				
SEQUENCE	62 AA; 7230 MW; 6BD1E04014CFAD8 CRC64;				
Query Match	78.1%; Score 25; DB 2; Length 62;				
Best Local Similarity	50.0%; Pred. No. 60; Mismatches 5; Indels 0; Gaps 0; Matches 5; Conservative 5; Score 25; DB 2; Length 62;				
Qy	1 EXEXFFXXXX 10				
Db	52 EAEDFFGSAE 61				
RESULT 4					
OS6T2Z0	PRELIMINARY;	PRT;	166 AA.	Qy	1 EXEXFFXXXX 10
ID	06T2Z0;			Db	52 EAEDFFGSAE 61
AC	AC06T2Z0;				
DT	05-JUL-2004 (TRMBLrel. 27; Created)				
DT	05-JUL-2004 (TRMBLrel. 27; Last sequence update)				
DT	05-JUL-2004 (TRMBLrel. 27; Last annotation update)				
DE	Cyclin-dependent kinase inhibitor 2 (Fragment).				
OS	Glycine max (Soybean).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Fabales; Fabaceae; Phaseoleae; Phaseoideae; Papilionoideae; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3847;				
RN	SEQUENCE FROM N.A.				
RA	Li S., Reverdatto S., Nielsen N.C.; "CLNA of cell-cycle genes in soybean coryledons,"				
RX	Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.				
RL	EMBL; AY439104; AAS13377.1; -.				
DR	DR				
KW	Cyclin-dependent kinase inhibitor 2 (Fragment).				
FT	NON TER 166 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;				
SEQUENCE	166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;				
Query Match	78.1%; Score 25; DB 2; Length 166;				
Best Local Similarity	50.0%; Pred. No. 1.6e+02; Mismatches 5; Conservative 5; Indels 0; Gaps 0;				
Qy	1 EXEXFFXXXX 10				
Db	127 ELEDFFAAAE 136				
RESULT 5					
OSAAS13377	PRELIMINARY;	PRT;	166 AA.	Qy	1 EXEXFFXXXX 10
ID	08AAS13377;			Db	127 ELEDFFAAAE 136
AC	AC08AAS13377;				
DT	10-MAY-2004 (TRMBLrel. 27; Last sequence update)				
DT	10-MAY-2004 (TRMBLrel. 27; Last annotation update)				
DE	Cyclin-dependent kinase inhibitor 2 (Fragment).				
OS	Glycine max (Soybean).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Fabales; Fabaceae; Phaseoleae; Phaseoideae; Papilionoideae; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3847;				
RN	SEQUENCE FROM N.A.				
RA	Li S., Reverdatto S., Nielsen N.C.; "Structural analysis of <i>Arabidopsis thaliana</i> chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty PI and TAC clones,"				
RX	PubMed=10819329;				
RL	DNA Res. 7:131-135 (2000).				
DR	DR				
RESULT 6					
OSQ9LY0	PRELIMINARY;	PRT;	189 AA.	Qy	1 EXEXFFXXXX 10
ID	09QLY0;			Db	127 ELEDFFAAAE 136
AC	AC09QLY0;				
DT	01-OCT-2000 (TRMBLrel. 15; Created)				
DT	01-OCT-2000 (TRMBLrel. 15; Last sequence update)				
DT	05-JUL-2004 (TRMBLrel. 27; Last annotation update)				
DE	Similarity to cyclin-dependent kinase inhibitor 5.				
DE	Name=KRP5;				
GN	Arabidopsis thaliana (Mouse-ear cress).				
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OC	NCBI_TaxID=3702;				
OX	NCBI_TaxID=3847;				
RN	SEQUENCE FROM N.A.				
RA	Li S., Nakamura Y.; "Structural analysis of <i>Arabidopsis thaliana</i> chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty PI and TAC clones,"				
RX	PubMed=20277480;				
RL	DNA Res. 7:131-135 (2000).				
DR	DR				
RESULT 7					
OSQ9LY0	PRELIMINARY;	PRT;	189 AA.	Qy	1 EXEXFFXXXX 10
ID	09QLY0;			Db	127 ELEDFFAAAE 136
AC	AC09QLY0;				
DT	05-JUL-2004 (TRMBLrel. 27; Created)				
DT	05-JUL-2004 (TRMBLrel. 27; Last sequence update)				
DT	05-JUL-2004 (TRMBLrel. 27; Last annotation update)				
DE	Cyclin-dependent kinase inhibitor 2 (Fragment).				
OS	Glycine max (Soybean).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Fabales; Fabaceae; Phaseoleae; Phaseoideae; Papilionoideae; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3847;				
RN	SEQUENCE FROM N.A.				
RA	Li S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.; "Structural analysis of <i>Arabidopsis thaliana</i> chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty PI and TAC clones,"				
RX	PubMed=10819329;				
RL	DNA Res. 7:131-135 (2000).				
DR	DR				

RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
RN	SEQUENCE FROM N.A. [3]	DE	Glycine max (Soybean); Cyclin-dependent kinase inhibitor 1;1.
RR	MEDLINE=21342516; PubMed=11449057;	OS	Glycine max (Soybean);
RA	de Veylder L., Beeckman T., Beemster G.T.S., Krots L., Terras F., Landrein I., Van Der Schueren E., Maes S., Naudts M., Inze D., "Functional analysis of Cyclin-dependent kinase inhibitors of Arabidopsis.", Plant Cell 13:1653-1668 (2001).	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Papilionoideae; Phaseoleae; Glycine.
RA	NCBI_TaxID=3847;	OC	
RA	RN [1]	OX	
RA	SEQUENCE FROM N.A.	RP	
RA	Li S., Reverdatto S., Nielsen N.C.; Li S., Reverdatto S., Nielsen N.C.; Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.	RA	
RL	EMBL; AJ301556; CAC41619..; -;	RL	
DR	GO; GO:0005634; C:nucleus; IEA.	DR	AY439101; AAS13374..; -
DR	GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a...; IEA.	DR	GO; GO:0016301; P:kinase activity; IEA.
DR	GO; GO:0016301; P:kinase activity; EA.	DR	InterPro; IPR003175; CDI.
DR	GO; GO:0007050; P:cell cycle arrest; IEA.	DR	Pfam; Pf02234; CDI; 1.
DR	InterPro; IPR003175; CDI.	DR	Cyclin; Kinase.
DR	PF0234; CDI; 1.	DR	
XR	Cyclin; Kinase.	SQ	SEQUENCE 205 AA; 22975 MW; 1B6F2D481710205E CRC64;
SEQUENCE 189 AA; 21424 MW; A66041310E8DDED6 CRC64;	Query Match	Match	Score 25; DB 2; Length 205;
SQ	Best Local Similarity 50.0%; Score 25; DB 2; Length 189;	Best Local Similarity	50.0%; Pred. No. 2+0+2;
Qy	Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	Matches	5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db	1 EXEXFXXXX 10	Qy	1 EXEXFXXXX 10
Db	148 EIEEFFAAAE 157	Db	164 EIEEFFAAAE 173
RESULT 9	AAS13374.. PRELIMINARY;	RESULT 9	AAS13374.. PRELIMINARY;
ID	QF0528	ID	QF0528
ID	QF0528.. PRELIMINARY; PRT; 192 AA.	AC	QF0528.. PRELIMINARY; PRT; 192 AA.
AC	QF0528.. PRELIMINARY; PRT; 192 AA.	AC	QF0528.. PRELIMINARY; PRT; 192 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Created)	DT	10-MAY-2004 (TREMBLrel. 27, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	DT	10-MAY-2004 (TREMBLrel. 27, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DT	10-MAY-2004 (TREMBLrel. 27, Last annotation update)
DI	Cyclin dependent kinase inhibitor.	DE	Cyclin-dependent kinase inhibitor 1;1.
GN	Name=chi;	OS	Glycine max (Soybean).
OS	Pisum sativum (Garden pea); Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Papilionoideae; Phaseoleae; Glycine.	OC	
OC	NCBI_TaxID=3847;	OC	
OC	RN [1]	RN	SEQUENCE FROM N.A.
OC	SEQUENCE FROM N.A. [1]	RA	Li S., Reverdatto S., Nielsen N.C.;
RN	RA	RT	"cDNA of cell-1-cycle genes in soybean cotyledons.";
RA	RA	RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RA	RA	DR	AY439101; AAS13374..; -
RA	RA	DR	
RA	SEQUENCE FROM N.A. [1]	SQ	SEQUENCE 205 AA; 22975 MW; 1B6F2D481710205E CRC64;
RA	RC TISSUE-Axillary bud; Shimizu-Sato S.; Mori H.;	Query Match	Match
RA	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	Best Local Similarity	50.0%; Pred. No. 2+0+2;
RL	EMBL; AB029483; BAB20860..; -;	Matches	5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
DR	GO; GO:0005634; C:nucleus; IEA.	Qy	1 EXEXFXXXX 10
DR	GO; GO:0004861; P:cyclin-dependent protein kinase inhibitor a...; IEA.	Db	164 EIEEFFAAAE 173
DR	GO; GO:0016301; P:kinase activity; IEA.		
DR	GO; GO:0007050; P:cell cycle arrest; IEA.		
DR	InterPro; IPR003175; CDI.		
DR	Pfam; PF02234; CDI; 1.		
RW	Cyclin; Kinase.		
SEQUENCE 192 AA; 21921 MW; E76D734000885EB2 CRC64;			
Qy	Query Match	RESULT 10	QGL00 PRELIMINARY;
Qy	Best Local Similarity 50.0%; Score 25; DB 2; Length 192;	ID	QGL00 PRELIMINARY;
Qy	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC	QGL00 PRELIMINARY;
Db	1 EXEXFXXXX 10	DT	05-JUL-2004 (TREMBLrel. 27, Created)
Db	151 EIEEFFAAAE 160	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
Db		DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
RESULT 8		DB	Hypothetical protein YCAQ
Q67223		GN	Name=YCAQ; Order=diocussNames=PBPB0166;
ID		OS	Photobacterium profundum (Photobacterium sp. (strain SS9));
Q67223	PRELIMINARY;	OC	Bacteriia; Proteobacteria; Gammaproteobacteria; Vibrionales;
ID	PRT; 205 AA.	OC	Vibrionaceae; Photobacterium; Photobacterium; Gammaproteobacteria; Vibrionales.
AC		OC	
DT	05-JUL-2004 (TREMBLrel. 27, Created)	NCBI_TaxID=74109;	
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	RN	SEQUENCE FROM N.A.
RP		RP	

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulio N., Lauro F.,
 RA Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D.,
 RA Valle G.;
 RT "Genome analysis of Photobacterium profundum reveals the complexity of
 high pressure adaptations";
 RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; CR37675; CAG2039.1; -;
 RN Complete proteome; Hypothetical protein.
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298EB9C9C57 CRC64;

Query Match Score 78.1%; Best Local Similarity 50.0%; Matches 5; Conservative 5; Mismatches 0; Pred. No. 2.2e+02; Length 223; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 189 EXETEFFTALE 198

RESULT 11
 CAG22039 PRELIMINARY; PRT; 223 AA.
 ID CAG22039; AC CAG22039; DT 10-MAY-2004 (TREMBLrel. 27, Created)
 DT 10-MAY-2004 (TREMBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein yCAQ.
 GN YCAQ OR PBPB016.
 OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrioaceae; Photobacterium.
 OX NCBI_TAXID=74109;
 RN SEQUENCE FROM N.A.
 RP STRAIN SS9;
 RC CAG22039; RT "Genome Analysis of Photobacterium profundum reveals the complexity of
 high pressure adaptations";
 RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL SEQUENCE FROM N.A.
 RC Cestaro A.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 KW Hypothetical protein.
 SQ SEQUENCE 223 AA; 25756 MW; F1DC29298EB9C9C57 CRC64;

Query Match Score 78.1%; Best Local Similarity 50.0%; Matches 5; Conservative 5; Mismatches 0; Pred. No. 2.2e+02; Length 223; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 189 EXETEFFTALE 198

RESULT 12
 Q7XDH8 PRELIMINARY; PRT; 242 AA.
 ID Q7XDH8; AC Q7XDH8; DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-MAR-2004 (TREMBLrel. 25, Last sequence update)
 DE Putative cyclin-dependent kinase inhibitor.
 GN ORFNames=OSJNBB009403.16;
 OS Orzya sativa (Japanese cultivar-group).
 OC Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
 OC Ehrhartoidae; Orzyeae; Orzya.
 OX NCBI_TAXID=39947;

RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 chromosome 10";
 RL Science 300:1566-1569 (2003).

[1] RN SEQUENCE FROM N.A.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 chromosome 10";
 RL Science 300:1566-1569 (2003).

[2] RN SEQUENCE FROM N.A.
 RA Bueli C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR AE01704; AAP54233.1; -;
 DR Gramene; Q7XDH8; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a...; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR InterPro; IPR03175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.
 KW Sequence 242 AA; 26750 MW; F215A0123473528 CRC64;

Query Match Score 78.1%; Best Local Similarity 50.0%; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 202 ELEAFFAAEE 211

RESULT 13
 Q9FW65 PRELIMINARY; PRT; 242 AA.
 ID Q9FW65; AC Q9FW65; DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative cyclin-dependent kinase inhibitor.
 GN Name=OSJNBB009403.16;
 OS Orzya sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Barthrioidace; Orzyea; Orzya.
 OX NCBI_TAXID=4530;
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Bueli C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C., Hsiao J., Zisman V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; DR Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RL SEQUENCE FROM N.A.
 RA Bueli R.; DR Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC069145; AAG16867.1; -;
 DR Gramene; Q9FW65; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a...; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; F:cell cycle arrest; IEA.
 DR InterPro; IPR03175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.

Query Match Score 78.1%; Best Local Similarity 50.0%; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EXEXFXXXXE 10
 Db 202 ELEAFFAAEE 211

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Query Match      Score 25; DB 1; Length 380;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 EXEXPXXXX 10
| |
| |
| |
| |
| |
3.30 ETESFQAKE 3.39

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